15:49:10 2004

Wed Mar

```
Sequence 43, Appl
Patent No. 5198359
Patent No. 549756
Sequence 20, Appl
Sequence 27, Appl
Sequence 7, Appli
Sequence 1, Appli
Sequence 15, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 87 CambridgePark Drive Inc.
STREET: 87 CambridgePark Drive STREET: 87 CambridgePark Drive STATE: MA COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM:
MEDIUM TYPE: BIOPPY disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BATCHIEN Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION NUMBER: US/09/040,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1195; DB 3; Best Local Similarity 100.0%; Pred. No. 1.5e-122; Matches 218; Conservative 0; Mismatches 0;
                                                                                                         US-09-313-942-20
US-09-313-942-22
US-09-313-942-30
US-08-078-311-7
US-08-460-402-7
US-08-184-327A-4
                             US-08-708-123D-43
US-08-638-524B-43
US-08-640-389A-12
                                                                                                                                                                                                                                    PCT-US95-00670-4
US-08-827-962-19
                                                                                                                                                                                                                                                                 US-08-827-962-15
                                                                                                                                                                                                    US-08-078-311-1
US-08-460-402-1
                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09040005
Patent No. 6057128
GENERAL INFORMATION:
APPLICANT: Donaldson, Debra
APPLICANT: Unger, Michelle
ITITLE OF INVENTION: MU-1 RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,724
mpR: GI5320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GIS3
TELECOMMUNICATION INFORMATION:
TELEFONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                          US-09-040-005-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-040-005-2
    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Appli
Sequence 115, App
Sequence 2, Appli
                                                                                                      March 3, 2004, 12:33:10 ; Search time 15:317 Seconds (without alignments) 734.770 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                    1195
1 CPDLVCYTDYLQTVICILEM.....SDPVIFQTQSBELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-404-641-2
US-09-223-246-115
US-09-523-217-97
US-09-522-217-97
US-09-923-246-97
US-09-923-246-97
US-09-973-246-97
US-09-748-859-6
US-09-784-859-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-08-583-153A-2
1-08-570-142D-2
3-08-638-524B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-599-455B-43
-09-069-781B-43
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-864-564A-2
                                                                                                                                                                                                                                                                               389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                     US-09-825-561A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
```

0

Gaps

õ 셤 ò

```
Sequence 1157 Application US/09923246 Patent No. 6605272 GENERAL INFORMATION:
   APPLICANT: No. 6576744ak, Julia E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-09-404-641-2
80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLABSIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                    SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 SDYEDPAFYMLKGKLÓYELÓYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELÓ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                      140 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSKSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1195; DB 4; Length 538; Best Local Similarity 100.0%; Pred. No. 1.5e-122; Matches 218; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Hollon, Janet V.
APPLICANT: Hammond, Anglew V.
APPLICANT: Hammond, Angelw K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND FILE REFERENCE: 99-16
CURRENT FILING DATE: 1090-03-09
CURRENT FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER PELLING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOSTWARE: FREESEQ for Windows Version 3.0
                                                                                                                                                                                                                                     181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2, Application US/09404641
). 6576744
```

ብ ò

```
80 TCHMDVFHFMADDIPSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 SDYEDPAFYMLKGKLOYELOYENRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSYELO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Prenell, Scott R.
APPLICANT: Prenell, Scott R.
APPLICANT: Specher, Cindy A.
APPLICANT: Specher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Welson, Jane V.
APPLICANT: Welson, Andrew J.
APPLICANT: Welson, Andrew J.
APPLICANT: Melson, Andrew J.
APPLICANT: Mammond, Angela R.
APPLICANT: Mammond, Angela R.
APPLICANT: WOVEL CYTOKINE ZAIPHAIL LIGAND
FILE REPRENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT PILING DATE: 2001-08-03
PRIOR PILING DATE: EAALIER FILING DATE: 2000-03-09
PRIOR PILING DATE: EAALIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EAALIER PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EAALIER PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EAALIER FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: EAALIER FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLARSIKPAPPFNYTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1195; DB 4; Length 538; Best Local Similarity 100.0%; Pred. No. 1.5e-122; Matches 218; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSERLKEGWNPH 218
FILE KEFEKENEE, 30-25
CURRENT PELLING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/100,896.
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-07-06
NUMBER: OF SEQ ID NOS: 91
SOFTWARE: PSECSEQ for Windows Version 3.0
SSOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO 2.
```

```
VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                         Sequence 97, Application US/09522217
Patent No. 6307024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-404-641-51
                                                                                                   RESULT 6
US-09-522-217-97
181
                                      200
                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                             ö
                                                                                                                                                                                                                             TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                        SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                     9
                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                   SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLBFRKDSSYELQ
                                                                                                                                            20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELXDEATSCSLHRSAHNATHATY
                                                                                                                                                                                       TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                     1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                          ..
0
               Query Match
100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 115, Application US/10295723

Patent No. 6686178

GENERAL INFORMATION:
APPLICANT: No. 6866178ak, Julia E.
APPLICANT: Presentl, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Hollon, Janet V.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
ITILE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND FILE REPERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                          VRAGPMPGSSYQGTWSEWSDPVIFQTQSBELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                  VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1195; DB 4; Best Local Similarity 100.0%; Pred. No. 1.5e-122; Matches 218; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/522,217
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FREUSEZ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-295-723-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 115
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                  19
                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                     à
                                                                                                                                         음
                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                    ਨੇ
```

```
448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 CPDLVCYTDYLQTVICILEMMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: MEP-zalphall soluble receptor polypeptide sequence US-09-522-217-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                 APPLICANT: Presnell, Soott R.
APPLICANT: Presnell, Soott R.
APPLICANT: Spreacher, Clindy A.
APPLICANT: Spreacher, Clindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Gross, Jane A.
APPLICANT: Gross, Jane A.
APPLICANT: Obnston, Janet V.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Angela K.
ITTLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND FILE REFERENCE: 99-16
CURRENT PLILNG DATE: 199-03-09
RAKLIER APPLICATION NUMBER: US 60/123, 904
BARLIER FILING DATE: 1999-03-09
RAKLIER FILING DATE: 1999-03-01
BARLIER FILING DATE: 1999-03-01
BARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 97
VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSBELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1195; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-122; Matches 218; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/09404641
Patent No. 657674
Patent No. 657674
Patent INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Conklin, Darrell C.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
FILE REFERRES: 98-55
CURRENT APPLICATION NUMBER: US/09/404,641
```

ö

ô

Gaps

```
121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                 61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                          509 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 CPDIVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLARSIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                          389 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 TCHMDVFHFMADDIPSVNITDQSGNYSQBCGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                            449 TCHMDVFHFWADDIPSVNITDQSGNYSQECGSFLLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPDLVCYTDYLQTVICILEMMNIHPSTLTLTUTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: MBP-zalphall soluble receptor polypeptide sequence
US-10-295-723-97
                                                                               ó
                           Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 606;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FOSTER, JOINING C.
APPLICANT: FOSTER, DORAID C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND FILE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND FILE OF THOR APPLICATION NUMBER: US/10/295,723
CURRENT APPLICATION NUMBER: US/05/21/7
PRIOR PLILING DATE: 1999-03-09
PRIOR PLILING DATE: 1999-03-09
PRIOR PLILING DATE: 1999-03-09
PRIOR PLILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR PLILING DATE: 1999-03-11
PRIOR PLILING DATE: 1999-03-11
PRIOR PLILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 1195; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0;
                     100.0%; Score 1195; DB 4;
100.0%; Pred. No. 1.8e-122;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97, Application US/10295723
Patent No. 6686178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: No. 6686178ak, Julia
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                  Query Match
Best Local Similarity 100.'
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLARSIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509 SDYEDPAFYMLKGKLOYELOYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELO 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Foster, Donald C.
APPLICANT: Foster, Jonald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Johnston, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
TILLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-03-03
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-07-01
NUMBER OF ENG ID NOS: 115
SOFTWARE: FARESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: MBP-zalphall soluble receptor polypeptide sequence US-09-923-246-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1195; DB 4;
Pred. No. 1.8e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR PILING DATE: 1998-09-03
PRIOR PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR PILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Fast SEQ for Windows Version 3.0
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97, Application US/09923246 Patent No. 6605272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: No. 6605272ak, Julia E. APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A. APPLICANT: Foster, Donald C. APPLICANT: Holly, Richard D. APPLICANT: Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n 100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

COTHER INFORMATION:

US-09-404-641-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ਨੇ
```

508

ö

g ઠે

us-09-825-561a-6.rai

```
Query Match
70.1%; Score 838; DB 4;
Best Local Similarity 68.3%; Pred. No. 2.4e-83;
Matches 149; Conservative 33; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INPORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. 6576744ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Mouse OCR10 protein US-09-784-859-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 81, Application US/09404641
Patent No. 6576744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 68.3%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-404-641-81
                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 TCHMRLSQFLSDEVFIVNVTDQSGNNSQECGSFVLAESIKPAPPLNVTVAFSGRYDISWD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYBLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 CLDLICYTDYLWTITCVLETRSPNPSILSLTWQDEYEBLQDQETFCSLHRSGHWTTHIWY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTMQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.6%; Score 844; DB 4; Length 529; Best Local Similarity 69.3%; Pred. No. 5.2e-84; Matches 151; Conservative 31; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT MURPHY, et al.

TILLE OF INVENTION: METHODS OF MODIFYING EUKARYOFIC CELLS
FILE REFERENCE: REG 780A
CURRENT PELLING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NO 6
LENGTH: 529
                                            569 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 VRAAPQPGTSFRGTWSEWSDPVIFQTQAGEPEAGWDPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                 APPLICANT: Presnell; Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. 65764448. Julia E.
APPLICANT: Hamond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAIL
FILE REPERENCE: 98 -55
CURRENT APPLICATION NUMBER: US/09/404,641
CURRENT PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR PILING DATE: 1999-07-06
NUMBER OF SEQ. ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Mouse OCR10 protein
                                                                                                                                                                Sequence 85, Application US/09404641
Patent No. 6576744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09732234
Patent No. 6586251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-09-732-234-6
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
```

g

ਨ੍ਹੇ

S

ጽ

⋩

```
140 SAYDEPSNYVIRGKLOYELQYRILRDPYAVRPVTKLISVDSRNVSLLPEEFHKDSSYQLQ 199
                                                                                                                                                                                                                                                                               80 TCHMRLSQFLSDEVFIUNVTDQSGNNSQEGGSFVLAESIKPAPPLNVTVAFSGRYDISWD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 TCHMRLSQFLSDEVFIVNVTDQSGNNSQEGGSFVLAESIKPAPPLNVTVAFSGRYDISWD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDYEDPAFYMLKGKLOYELOYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 CLDLTCYTDYLWTITCVLETRSPNPSILSLTWQDBYBELQDQBTFCSLHKSGHNTTHIWY 79
                                                                                                                                                                                                                                           61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                   1 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYBBLKDBATSCSLHRSAHNATHATY
                                                                                                                                                                                  CLDLTCYTDYLWT1TCVLETRSPNPS1LSLTWQDEYBELQDQETFCSLHKSGHNTTH1WY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09784859

Batent No. 6596541

GENERAL INFORMATION:

APPLICANT: MULTPA, et al.

FILE REPRENCE: REG 780B

CURRENT APPLICATION HOBER: US/09/784,859

CURRENT FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.0

SEQ ID NO 6

LENGTH: 529
Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.1%; Score 838; DB 4; Length 529; 68.3%; Pred. No. 2.4e-83; ive 33; Mismatches 36; Indels
                                                    36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VRAGPMPGSSYQGTWSEWSDPVIPQTQSBELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 MRAAPQPGISFRGIWSEWSDPVIFQIQAGEPEAGWDPH 237
```

```
TOPOLOGY: Linear
           ;
US-08-780-562-7
                                                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                        셤
                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 QYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.5%; Score 400; DB 4; Length 397; Best Local Similarity 68.6%; Pred. No. 1.9e-35; Matches 72; Conservative 18; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 DSSYELOVRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DSSYQLQMRAAPQPGTSFRGTWSEWSDPVIFRTQAGEPEAGWDPH 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/09/404,641
CURRENT PILLING DATE: 1999-09-23
FRIOR APPLICATION NUMBER: US 60/100,896
PRIOR PILLING DATE: 1988-09-23
PRIOR PILLING DATE: 1999-03-09
PRIOR PILLING DATE: 1999-03-09
PRIOR PILLING DATE: 1999-07-06
PRIOR PILLING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
NUMBER OF SEQ ID NOS: 91
NUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET 466 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Genetical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P0986R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLICATION: 435
PLICAR APPLICATION DATA:
PRICAL APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRICA APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELEFONE: 415/25-1994
TELEFAX: 415/95-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 anino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08780562
Patent No. 6541604
                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-404-641-81
                                                                                                                                                                                                                                      SEQ ID NO 81
LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

```
; TOPOLOGY: linear
; MOLBCULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-599-4558-2
```

Query Match
12.1%; Score 144; DB 2; Length 894;
Best Local Similarity 31.1%; Pred. No. 7.9e-07;
Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11; 39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS 87 ሯ ન

ጵ

8 ጵ

a

유 ⋩ Search completed: March 3, 2004, 12:39:55 Job time: 15.317 secs

```
homo sapien
mus musculu
mus musculu
mus musculu
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
rattus norv
homo sapien
homo sapien
macaca mula
rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mus musculu
mus musculu
sus scrofa
bos taurus
canis famil
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
homo sapien
homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gallus gall
rattus norv
                                                                                                                                    March 3, 2004, 12:25:04; Search time 8.19281 Seconds (without alignments) 1385.519 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                            218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                         CPDLVCYTDYLQTVICILEM.....SDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099163

099163

099163

099163

099163

099163

099163

099178

099178

099178

099178

099178

099178

099178

099966

099966

099966

099966

099966

099966

099966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9hbe5
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                           141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
CHICK
RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
MOUSE
MOUSE
MOUSE
MOUSE
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
MACMU
RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
MOUSE
PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
MELGA
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOVIN
                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121R | 121R | 121R | 121R | 123B | 122B | 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L4R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                             US-09-825-561A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SwissProt_42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5538

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

10895

108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pitle:
Perfect score:
                                                                                                                                                                                                                                                                                                                        scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ainimum DB seq
Aaximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118
117
115.5
                                                                                           ì
                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jatabase :
                                                                                                                                                                                                                                                                            sequence:
                                                                                                                                                                                                                                                                                                                                                                                             searched:
                                                                                                                                       sun on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lesult
```

Q01113 homo sapien P19941 oryctolague P19235 homo sapien Q01114 mus musculu Q18796 sus scrofa P14753 mus musculu Q01344 homo sapien P42701 homo sapien P22273 rattus norv P21183 mus musculu Q28235 cervus elap P48095 macaca mula	s. AA.	<pre>uence update) iotation update) sor (IL-21R) (Novel interleukin Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.</pre>	N FIGURE FROM N.A. KEDLINE-20531754; PubMed=11081504; REDLINE-20531754; PubMed=11081504; R Parrish.Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., B Burkhead S., Heipel M., Brandt C., Kuijper J.L., Kramer J., R Burkhead S., Heipel M., Berry J., Shicta F., Bort S., Hambly K., A Mudris S., Clegg C., Moore M., Grant F.J., Lofton-pay C., Gilbert T., R Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Manver M., Kaushansky K., Holly R.D., Foster D., "Interleukin 21 and its receptor are involved in NK cell expansion and I regulation of lymphocyte function.";	Wed=11016959; foung P.R., Leonard W.J.; cytokine receptor most related to the IL-2 cytokine receptor most related to the IL-2. U.S.A. 97:11439-11444(2000). $0 \in \mathbb{C}_n^{-1} \in \mathbb{C}_n^{-1}$ U.S.A. 97:11439-11444(2000). $0 \in \mathbb{C}_n^{-1} \in \mathbb{C}_n^{-1}$ X. Carington D.P., Chung MW., Lee K.L., Yi Q., Nickerson D.A.; to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. TISSUE=22388257; PubMed=12477932; KISJUE=22388257; PubMed=12477932; Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G., A Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D., A Altschul S.F., Jordan H., Moore T., Mans S.I., Wang J., Haiteh F., Hopkins R.F., Jordan H., Moore T., Mars S.I., Wang J., Haiteh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., A Scaptes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
ILSR HUMAN GHR RABIT EPOR HUMAN ILISA MOUSE ILISA MOUSE ILISA HUMAN ILISR HUMAN ILISR HUMAN ILISR HUMAN ILISR MOUSE ILISR MOUSE PRIR CERREL	ALIGNMENTS PRT; 538	nuence update) lotation update) reor (IL-21R) (Nc. Craniata; Verte) Catarrhini; Hom	.504; Nelson A. Nelson A. C., Xu W C., Kuijp Cry J., Shi Grant F.J. Smith D., Y R.D., Fo	Pubwed=11016959; Michalowich D., Young P.R., Le i I cytokine receptor most relate n."; Sci. U.S.A. 97:11439-11444 (2000) , AND VARIANTS CYS-191; ARG-318 T.Z., Carrington D.P., Chung M. J., Yi Q., Nickerson D.A.; J., to the EMBL/GenBank/DDBJ data	932; Grouse L., Grouse L., E.O., K.H., E.O., K.H., G.O., G.O., Coshiyuki S. Eres G.U., Coshiyuki S. Coshiyuki
	а т ф	it, Last section is the control of t	=11081 S.R., Madde Brandte, Ber M., D.L., Holl recept	bmed=1101695 Michalovich 5 Cytokine re ", v. s. 97 i. U.S.A. 97 i. U.S. Carring ' Yi Q. Nicolic to the EMBL	; = 12477 d E.A. S.Y. W. Noore K., Bon J. Bon J. P. P. MCKer Hale , Sod teman
000440404406 00000000000000000000000000	NDARD; HB91;	#1, La #3, La eptor n). Chor	Pubmed Dillon Dn J., Il S.R Moor A., Yak A., Yak A., Yak	PubMed= . Micha I."; sci. U. Sci. U. T.Z., I., Yi	Lymph PubMed Pingol Lins F Lins F An H., An H., Lsina Bsd M.B Sdin T Bodin T P.J., K.C.
######################################	STAN HZ1, Q9E	(Rel. (Rel. LR. Recent of the	OM N.A. 31754; I ak J., I Johnstc , Heipel Presnel legg C., Ching Y Kaushans n 21 anc	OM N.A. 81926; I ikly K., a type ta chair Acad. 8 OM N.A., Armel Toth E.	FROM N.Acell, and -cell, and rg R.L. FR.D. Coll S.F., Zeek S.F., Dord K. L., Mar. n. M., Soare n. M., Soare n. M., McBwan S., Worley D.K., Muzz C.K., Muzz K., Muz
105 104 103 103 103 99 99 95 95 95	r 1 HUMAN 121R HUMAN QQHBES; Q96	28-FEB-2003 (Rel. 4), Last sequence 15-MAR-2004 (Rel. 43, Last amotatio Interleukin 21 receptor precursor (I receptor). IL21R OR NILR. Homo saplens (Human). Bikaryota; Metazoa; Chordata; Crania Mammalia; Butheria; Primates; Catarr NCSI_TAXID=9606;	UDUCENCE FREGUENCE FREGUENCE FREGUENCE OSSINITATION	SEQUENCE FROM N.A. MEDLINE-20481926; PubMed=11016959; Ozaki K., Kikly K., Michalowich D., YC "Cloning of a type I cytokine receptor receptor beta chain."; Proc. Natl. Acad. Sci. U.S.A. 97:11435 [3] SEQUENCE FROM N.A., AND VARIANTS CYS-18 Reder M.J., Armel T.Z., Carrington D. Poel C.L., Toch E.J., Y Q., Nickersor Submitted (NOV-2001) to the EMBL/GenBE	SEQUENCE FR TISSUB=B-ce MEDLINE=223 Krauuser R. Altschul S. Hopkins R.F. Diatchenko Stapleton M Stapleton M Brownstein Raha S.S., Richards S.S., Villalon D. Fahey J., H
₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	34 18 4	SX SEE IT IT IS SX	RRY RRY MS I I I I I I I I I I I I I I I I I I	RR	A STANDARD OF THE STANDARD OF

homo sapien homo sapien sus scrofa mus musculu

P19756 P22272 P16310

Q00560 P40189 P08887

MOUSE HUMAN HUMAN

115 112.5 110.5 108.5 106 106.5

L6B

meleagris g mus musculu mus musculu

80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                     with JAKI.
-- SUBGELLULAR LOCATION: Type I membrane protein.
-- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.
Most highly expressed in thymus and spleen.
-- SIMILARITY: Belongs to the type I cytokine family of receptors.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. US.A. 9916899-16903(2002).
-!- FUNCTION: This is a receptor for interleukin-21.
-!- SUBUNIT: Heterodimer with the common gamma chain. Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTIG=VAR 014362.
AVP -> HEA (IN REF. 4; AAH07946)
G -> R (IN REF 2)
414079CCB974850A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO1355; HEMATOPO REC S F1; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; GO:0030101; F:Interleukin-21 receptor activity; NAS. InterPro; IPR003961; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR 014360.

S -> R (in dbSNP:3093385).

/FTId=VAR 014361.

G -> S (in dbSNP:3093386).
                                                                                                                                                                                                               Subfamily 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERLEUKIN 21 RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R -> C (in dbSNP:3093370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1195; DB 1;
; Pred. No. 1.1e-96;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 605383; -.
GO:0016021; C:integral to membrane; NAS.
GO:0001532; F:interleukin-21 receptor ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR003531, Hemtopoptn_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF254067; AAG29346.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF269133; AAG33419.1; --
EMBL; AY064474; AAL39168.1; --
EMBL; BC004348; AAH04348.1; --
EMBL; BC007946; AAH07946.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59129 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:6006; IL21R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 3
538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00060; FN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMAIN
```

```
140 SDYEDPAFYMLKGKLOYELOYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE=20531754; PubMed=11081504;

MEDILINE=20531754; PubMed=11081504;

Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xuw., West J., Schrader S., Burkhead S., Heipel M. Gaden C., Kuijper J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hambly K., Mudri S., Clegg C., Moore M., Grant P.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D., Interleukin 21 and its receptor are involved in NK cell expansion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-A/J, B10.S/DvTe, C57BL/6J, NOD/LtJ, and SJL/J; TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | with JAKI.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridäe, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gao J., Teuscher C.;
"Mus musculus interleukin 21 receptor gene 1121r mRNA.";
"Mus musculus interleukin 21 receptor gene 1121r mRNA.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
-1. FUNCTION: This is a receptor for interleukin-21.
-1. SUBUNIT: Heterodimer with the common gamma chain. Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Spleen, and Thymus;
MEDLINE=20481926; PubMed=11016959;
Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
"Cloning of a type I cytokine receptor most related to the IL-2 receptor beta chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finnerty H.,
Dagdigian C., Lowe L., Wood C.R., Young D.A., Collins M.,
"Chromosome 16p12 encodes a biologically active IL-2Rb related
"receptor with lymphoid restricted expression.",
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               Q9JHX3; Q9RSM1;
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
11-MAR-2004 (Rel. 43, Last annotation update)
11-21R (Novel interleukin receptor beta) (LR-beta) (Novel cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
A novel Cytokine receptor NR8.is closely mapped to IL-4R:
polymorphism in Balb/c mouse "".
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                      218
                                                                                                                     200 VRAGPMPGSSYĞGTWSEWSDPVİFQTQSBELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444 (2000).
                                                                                      181 VRAGPMPGSSYQGTWSEWSDPVIFOTOSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation of lymphocyte function.";
Nature 408:57-63 (2000).
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gao J., Teuscher C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                   receptor NR8)
                                                                                                                                                                                                                                               21R MOUSE
                                                                                                                                                                                                                                                                    à
                                 셤
                                                                                      8
                                                                                                                                 셤
```

ö

Gapa

ö

Indels

TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDBATSCSLHRSAHNATHATY 79 CPDLVCYTDYLOTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY

20

g ઠ

61

```
27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2
                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
463
39
254
293
69
350
350
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                       + + +
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCHMRLSQFLSDEVFIVNVTDQSGNNSQEGSFVLASSIKPAPPLNVTVAFSGRYDISWD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAYDEPSNYVLRGKLÖYELÖYRNLRDPYAVRPVTKLISVDSRNVSLLPEEFHKDSSYQLQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDBATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLDLTCYTDYLWTITCVLETRSPNPSILSLTWQDBYZELQDQETFCSLHRSGHNTTHIWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Most highly expressed in thymus and spleen.
SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
R -> K (IN STRAINS BALB/C AND SJL/J)
V -> M (IN STRAINS BALB/C AND SJL/J)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEMATOPO REC_S_F1; FALSE_NEG.
Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.6%; Score 844; DB 1; Length 529;
69.3%; Pred. No. 4.1e-66;
iive 31; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                 INTERLEBRIN 21 RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
PY SIMILARITY.
POTENTIAL.
                        Subfamily 4.
SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8B41816B0D426581 CRC64;
                                                                                                                                                                                          EMBL; AF477982; AAL82632.1; -...
EMBL; AF477983; AAL82633.1; -...
EMBL; AF477984; AAL82634.1; -...
EMBL; AF477985; AAL82554.1; -...
EMBL; AF477985; AL82556.1; -...
EMBL; AF4779875; Illzr.
GO; GO:0004907; F:interleukin receptor activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR008957; FW III-like.
InterPro; IPR003961; FW III.
InterPro; IPR003531; Hemtopoptn_S_F1.
                                                                                                                                                 EMBL; AF254068; AAG29347.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58354 MW;
                                                                                                                                                         EMBL; AF269134; AAG23420.1
EMBL; AF279436; AAF86350.1
EMBL; AB049137; BAB13736.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 69.3%
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
200
529 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
IL3B MOUSE
ID IL3B MOUSE
AC P26954;
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>유</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

Æ

PRT;

STANDARD;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                        MEDITE=90171145; PubMed=2404337; Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A., Yahara I., Arail K., Miyajima A.; "Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene family."; Science 247:324-327(1990).

-I. FUNCTION: In mouse, there are two classes of high-affinity IL3 receptors. One contains this IL3-specific beta chain and the other contains the beta chain also shared by high-affinity IL5 and GM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 HMDVFHFMADDIFSVNITDQSGNYSQECGSFLLA-ESIKPAPPFNVTVTFSGQYNISWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 DLVCYTDYLQTVICILEMMNLHPSTLTLTWQDQYBELKDBATSCSLHRSAHNATHATYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSF receptors.
SUBUNIT: Heterodimer of an alpha and a beta chain.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).

POTENTIAL.
CYPODIASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N SIMILARITY.
N LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
01-OCT-1993 (Rel. 27, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
InterNeukin-3 receptor class II beta chain precursor (Colony stimulating factor 2 receptor, beta 2 chain).
CSF2RB2 OR AI2CA OR II3RB2 OR II3R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 145; DB 1; Length 878; 23.0%; Pred. No. 6.2e-05; ive 38; Mismatches 97; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERLEUKIN-3 RECEPTOR CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8EBC9092ADC24D56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S01355; HEMATOPO REC_S_F1; 1.
Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEL, M29855, AAA39295.1; --
PTR: A40091, A40091.
MGD, MGI.1339760, Cef2rb2.
INTERPRO, IPR002996, CRIA.
INTERPRO, IPR002882, Cytok receptor_2.
INTERPRO, IPR003981, FW III-11ke.
INTERPRO, IPR003981; FW III-11ke.
INTERPRO, IPR003981; FW III-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97195 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01355; HEMATOPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity 23.0%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A PART OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ጵ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90319131; PubMed=1695379;
A Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
A Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
Yahara I., Arai K., Miyajima A.;
"Cloning and expression of a gene encoding an interleukin 3 receptor—
It like protein: identification of another member of the cytokine
receptor gene family."; Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
C. - FUNCTION: High affinity receptor for interleukin-5
and granulocyte-macrophage colony-stimulating factor.
C. - SUBGELLULAR LOCATION: Type I membrane protein.
C. - SUBGELLULAR LOCATION: Type I membrane protein.
C. - SUBGELLULAR LOCATION: Type I membrane protein.
C. - SUMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 4.
C. - SIMILARITY: Contains 2 fibronectin type III domains.
                                                         365 QKIPKYIDHTF------QVQYKKKKSESWKDSKTENLGRVNSMD---LP-QLEPDISY 411
        D----YEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cytokine receptor common beta chain precursor (CDw131 antigen) (GM-CSF/IL-3/IL-5 receptor common beta-chain).

GRF/IL-3/IL-5 receptor common beta-chain).

Mus musculus (Mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUENCHIALLY
FYTOPLASHIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M34397; AAA37204.1; -.
PIR; A35782; A35782.
MGD; MG1:1339782; C8f2rb1.
InterPro; IPR002996; CRIA.
InterPro; IPR00396; Cytok receptor_2.
InterPro; IPR00396; FN III-like.
InterPro; IPR00351; Hemtcopoptn_S_P1.
SMART; SM00060; FN3; 2.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
Receptor; Transembrance; Glycoprofeth; Sepent; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOKINE RECEPTOR COMMON EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 896 AA
                                                                                                                                                                                                                       178 ELQVRAGPMPGSSYQGTWSEWSDPVIFQT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4416
224416
224444
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
25542
2554
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYRB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                     CYRB MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A PART TO THE TENT TO DESCRIPT TO THE PROPERTY TO THE PART TO THE 
                                                                                   В
                                                                                                                                                                   ò
```

```
300 PGASUYTRYHCSLPVPEPSAHSQYTVSVK-----HLEQGKFIMSYNHIQMEPPTLNLTK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 TFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVŞLLPL 169
                                                                                                                                                                                                                                               3 DLVCYTDYLQTVICILEMWN-------LHPSTLTLTWQDQYEELKDEATSCSLHRS
                                                                                                                                                                                                                                                                                                             250 NLQCFFDGIOSLHCSWEVWTOTTGSVSFGLFYRPSPVA------PEEKCSPVVKEP
                                                                                                                                                                                                                                                                                                                                                                        52 AHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLA-ESIKPAPP-FNVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Choroid plexus;
MEDLINE=56128129; PubMed=8548812;
Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
Mur C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;
"Identification and expression cloning of a leptin receptor, OB-R.";
Cell 83:1263-1271(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS A, B, C, D AND E).
STRAIN=CFSPLKS; ITSSUE=Hypothalamus;
MEDLINE=96231997; PubMed=8628931,
Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
Lee J.I., Friedman J.M.;
Abnormal splicing of the leptin receptor in diabetic mice.";
Nature 379:632-635(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS7BL/KsJ; TISSUE=Hypothalamus;
MEDLINE=S6190816, PubMed=8608603,
Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
Blyk G.M., Tepper R.I., Morgenstern J.P.,
"Byddence that the albetes gene encodes the leptin receptor: identification of a mutation in the leptin receptor gene in db/db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%; Score 144; DB 1; Length 896; 22.6%; Pred. No. 7.7e-05; tive 41; Mismatches 87; Indels
                                          BCE16EDFDC07A999 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.
Mikhail A., Platika D., Snodgrass H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 EFRKDSSYELOVRAGPMPGSSYQGTWSEWSDPVIFQT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=96206286; PubMed=8616721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [4]
SEQUENCE FROM N.A. (ISOFORM C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM A)
      141 141 N.
350 350 N.
896 AA; 99111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM B)
                                                                                                                                                      Local Similarity 22.6%
es 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 84:491-495(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10090;
```

Ŋ

"Novel B219/OB receptor isoforms: possible role of leptin in hematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).

```
1. ENORTION: Receptor for obseity factor (leptin). Involved in the regulation of fat metabolism and in a hematopoietic pathway regulation of fat metabolism and in a hematopoietic pathway regulation for normal lymphopoiesis. May play a role in reproduction.

-I FUNCTION: The short form (isoform A) may act to transport leptin to the cerebrospinal fluid. The putative soluble receptor (isoform E) could function as a transport protein.

-I SUBSELLULAR LOCATION: Type I membrane protein. Except for form E which could be secreted.
[5]
SEQUENCE FROM N.A. (ISOFORM B).
SEQUENCE FROM N.A. (ISOFORM B).
SEQUENCE TO TISSUE-Hypothalamus.
MEDLINE-97462708; PubMed-9222935;
IGel M., Becker W., Herberg L., Joost H.G.;
"Hyperleptinemia, leptin resistance, and polymorphic leptin receptor in the New Zealand obese mouse.";
Endocrinology 138:4234-4239(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skoda R.C.; "Defective STAT signaling by the leptin receptor in diabetic mice."; Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Banks A.S., Myers M.G. Jr.; "Murine leptin receptor genomic exon 18b and surrounding sequence."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese, hyperinsulinemic KK mouse strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION OF TYR-985 AND TYR-1138, AND MUTAGENESIS OF TYR-985,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYR-1077 AND TYR-1138. MEDLINE-2026.1888; PubMed-10799542; MEDLINE-2026.1888; PubMed-10799542; Banks A.S., Davis S.M., Bates S.H., Myers M.G. Jr.; "Activation of downstream signals by the long form of the leptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/J;
MEDLINE=98008913; PubMed=9344648;
MEDLINE=98008913; PubMed=9344648;
Chua S.C., Koutras I.K., Han L., Liu S.M., Kay J., Young S.J.,
Chung W.K., Lebbel R.L.;
"Fine structure of the murine leptin receptor gene: splice site
suppression is required to form two alternatively spliced
transcripts.";
Genomics 45:264-270(1997).
                                                                                                                                                                                                                                                                                              [6]
SEQUENCE FROM N.A. (ISOFORMS A AND B).
STRAIN=FVB/N; TISSUE=Spleen;
STRAIN=F96270520; PubMed=8692797;
Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT ASN-600.
STRAIN=KR Obese; TISSUE=Mypothalamus;
MEDLINE=99061614; PLMAGE=9845674;
Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=P48356-2; Sequence=VSP_001697, VSP_001698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P48356-4; Sequence=VSP_001701, VSP_001702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSP_001700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=P48356-5; Sequence=VSP_001703, VSP_001704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS A; B; C AND E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [9]
SEQUENCE OF 890-1162 FROM N.A. (ISOFORM B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P48356-3; Sequence=VSP_001699,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P48356~1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinol. 21:337-345(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE SPECIFICITY: Isoform A: highest level of expression in lung and kidney, also present in kidney, heart, brain, spleen, liver, muscle, choroid plexus end hypothalamus. Isoform B: highest level of expression in hypothalamus and lower level in brain, testes and adipose tissue. Isoform E: expressed in adipose tissue, heart, and testes.

PTM: Phosphorylated on two tyrosine residues. Tyr-985 may be the major site of phosphorylation. Phosphorylation on both sites is required for full activity.
                                                                                             Subfamily 2.
-!- SIMILARITY: Contains 3 fibronectin type III domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
JOINED.
ALT TERM.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                      JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                   COINED
                                                                                                                                                                                                                                                                                                                                                                                                                              COINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED
                                                                                                                                                                                                          EMBL; U42467; AAA93014.1; -.
EMBL; U46135; AAC52408.1; -.
EMBL; U49106; AAC52420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95335.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB95333.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAB95334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB95333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB95333.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB95334
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB95334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB95333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB95333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB95333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB95333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB95333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB95333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB95333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95333
                                                                                                                                                                                                                                               AAC52422.1
AAC52423.1
AAC52424.1
                                                                                                                                                                                                                                                                                     CAA71343.1
                                                                                                                                                                                                                                                                                                      US8862; AAC52706.
US8863; AAC52707.
                                                                                                                                                                                                                                                                         AAC52599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF039448;
                                                                                                                                                                                                                                                 U4910B;
                                                                                                                                                                                                                                                                            U52915;
                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                             MBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
```

INTERLEUKIN-2 RECEPTOR BETA CHAIN

ဖ

à 쉽 à g g à

à

```
racinis, PSO1355; HEMATOPO REC_SF1; 1.
Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1.
                                 HSSP; P14784; IILM.
MGJ; MGI:96550; Il2rb.
InterPro; IPR002996; CRLA.
InterPro; IPR003961; FN III-like.
InterPro; IPR003961; FN III-like.
InterPro; IPR003531; Hemtopoptn_S_F1.
                                                                                                                                                                                                                        Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEMATOPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPL OR TPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPOR HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 T--IVREAARIVSATSLLVDSVLP----GSSYEVOVRSKRLDGS---GVWSDWSSPQVF 326
                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90175385; PubMed=2155425,
A Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsudo M.,
A Miyasaka M., Miyata T., Taniguchi T.;
A Miyasaka M., Miyata M., Miyata M., Minamediate affinity forms also associate with a gamma chain.
C --- SUBCELLULAR LOCATION: Type I membrane protein.
C --- SUBCELLULAR LOCATION: Type I membrane protein.
C --- SUBCELLULAR LOCATION: Type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                      39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPWAVSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Interleukin-2 receptor beta chain precursor (IL-2 receptor) (F70-75)
ILLERIA affinity IL-2 receptor beta subunit) (CD122).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butéleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                     Length 1162;
                                                                                                                                                                                                                                                                                                                                                      60; Indels
                                                                                                                                                                                                                                                                                         12.1%; Score 144; DB 1;
31.1%; Pred. No. 0.00011;
ive 22; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539 AA
                                 COINED.
COINED.
COINED.
COINED.
COINED.
                                                                                                                                                                                                                               JOINED
AAB95335.1; UAB95335.1; UAB9535.1; UAB95535.1; U
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.1%;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Subfamily 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 QTQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTQ 329
                                                                                                                                                                  AF039454;
AF039455;
                                                                                                                                                                                                                               AF039456;
                                                                                                                                       AF039453;
                                                                                                         AF039452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL2B MOUSE
P16297;
                                                                       EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L2B MOUSE
```

```
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :: | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCHMDVFH-------FMADDIFSVNIT--DQSGNYSQECGSFLLAESIK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 SVLSLKOROOWLFLEMLIPSTSYBVOVRVKAORNNT--GTWSPWSOPLTFRTRPADPMKE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 PAPPENVIVIF--SGOYNISWR----SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thrombopoietin receptor procursor (TPO-R) (Myeloproliferative leukemia protein) (C-mpl) (CD110 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 CSHLECFYNSRANVSC----MWS-HEEALNV------TTCHVHAKS-NLRHWNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 KLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQ-SEELKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYBBLKDBATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and characterization of MPL, the human homolog of
the v-mpl oncogene: identification of a member of the hematopoietic
growth factor receptor superfamily.",
Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDILINE-23132231, PubMed=1608974;
Vigon I., Mornon J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
Gisselbrecht S., Souyri M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                (GLCNAC. ) (POTENTIAL)
(GLCNAC. ) (POTENTIAL)
(GLCNAC. ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POT
                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (Po
N-LINKED (GLCNAC. . .) (Po
365C9D206E86FE14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.8%; Score 141.5; DB 1
22.5%; Pred. No. 6.8e-05;
tive 43; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=94292186; PubMed=8020956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60538 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similaricy
nes 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
```

EMBL; M28052; AAA39283.1; -.

THE HERE WAS COOCCOUNTER THE TRANSPORT OF THE TRANSPORT O

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as lus content to commercial modified and this statement is not removed. Usage by and for commercial modified and this statement (see http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
                                                                                                                                                                                                                                                                                                          "Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Genet. 23:373-373 (1999).

-!- FUNCTION: Receptor for thrombopoietin. May represent a regulatory molecule specific for TPO-R-dependent immune responses.

-!- SUBCELLUIAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                  MEDLINE=99318093; PubMed=10391209; Cargll M., Ardlie K., Patil N., Cargll M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 2 fibronectin type III domains.
CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
DATABASE: NAME=PROW; NOTE=PROW 1:22-25(2000);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/11586825_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
Mignotte V., Vigon I., Boucher de Crevecoeur E., Romeo P.-H., Lemarchandel V., Chretien S., "Structure and transcription of the human c-mpl gene (MPL).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08424.1; JOINED.
AAB08424.1; JOINED.
AAB08424.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M90102; AAA69971.1; -.
                                                                                                                                                                                                                                                                                                                                                                  Nat. Genet. 22:231-238(1999)
                                                                                                                                          VARIANTS VAL-58 AND LYS-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB08425.1;
AAB08425.1;
AAB08425.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0008283; P:cell pro
GO; GO:0007166; P:cell sur
InterPro; IPR002996; CRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB08424.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB08425.1;
                                                                                     Genomics 20:5-12(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC: 7217; MPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U68162, AAB0842:
EMBL, U68169, AAB0842:
EMBL, U68160, AAB0842:
EMBL, U68161, AAB0842:
PIR, A45266, A45266.
PIR, B45266; B45266.
HSSP, P19235, 1EBA.
                                                                                                                                                                                                                                                                                                                                          of human genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew, HGNC:7
MIM; 159530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
```

```
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCFTLDLKNVTC--------OWOOO-----DHASSQGFFYHSRARCCPRDRYP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 LLAESIK-PAPPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG-DPWAVS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                                                                                                                         BPSLLEILPKSSERTP -> YRPROAGDWRWTRWSRTCKOA
FLVRSVTPDLRPPPVRTYGFALPARHLWDSPRLLTL (in
                                                                                                                                                                                                                                                                                           RLRHALWPSLPDLHRVLGQYLRDTAALSPPKATVSDTCEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRKLISVDSRSVSLLP-----LEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TCHM----DVFHFMADDIPSVNITDQSGNYSQECGS-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 IWENCEEEEKTNPGLQTPQFSRCHFKSRNDSIIHIL-----VEVTTAPGTVHSYLGSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 WIHQAVRLPTPNLHWREISSGHLELEW----QHPSSWAAQ-ETCYQLRYTGEGHQDWKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LVCYTDYLQTVICILEMMNLHPSTLTLTWQDQYEELKDEATSCSL--HRSAHNATHATY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                           PROSITE; PS01352; HEMATOPO REC_L_F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing; Stepat; Antigen; Polymorphism and 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEPR RAT STANDARD; PRT; 1162 AA.

Q62959; O35772; O35773; O54805; P70493; P70494; P70495; P97589; Q62950; Q62960; Q63007; Q63385; Q63386; Q9ERI4;
15-UIL-1999 (Rel. 38, Created)
15-UIL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-Dith receptor precursor (LEP-R) (OB receptor) (OB-R).
                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.6%; Score 139; DB 1; Length 635;
Best Local Similarity 24.0%; Pred. No. 0.00014;
Matches 59; Conservative 25; Mismatches 76; Indels
                                                                                                                       THROMBOPOIETIN RECEPTOR. EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TId=VAR 011989.
D25D8D8959359DDC CRC64;
                                                                                                                                                            POIGNIANTS

EY SIMILARITY

BY SIMILARITY

BY SIMILARITY

BY SIMILARITY

BY SIMILARITY

N-LINEED (GLCNAC. . ) (F

N-LINEED (GLCNAC. . ) (F

N-LINEED (GLCNAC. . ) (F
                                                                                                                                                                                                                                                                                                                                                             1881ng (In isoform 2).
Prid=VSP 001735.
A -> V (in dbSNP:6087).
Frid=VAR_011988.
                                                                                                                                                                                                                                                                                                                                                                                              /FIId=VAR_011988.
F -> K (in dbsNP:6088).
/FIId=VAR_011990
                                                                                                                                                                                                                                                                                                                                                    001734.
                                                                                                                                                                                                                                                                                                                                      isoform 2)
                                                                                                                                                                                                                                                                                                                                                       Id=VSP
             InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_Fl.
Pfam; PR00041; fn3; 2.
SMART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                    Missing
 interPro; IPR008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  71244 MW;
                                                                                                                                      491
513
635
                                                                                                                                                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 PQTQSE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 VETATE 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 AA;
                                                                                                                                                                                                                                                                                                                                                                   580
                                                                                                                                                                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                   TRANSMEM
                                                                                                                                                                                DISULPID
                                                                                                                                                                                                                                       CARBOHYL
                                                                                                                                                                                                            DISULFI
                                                                                                                                                                                                                                                    CARBOHYI
                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                       DOMAIN
                                                                                                                                                                    DOMAIN
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
```

```
(fa/fa) rat.
```

D85558; BAA12831.1; D85559; BAA12832.1; U60151; AAB06616.1; D84125; BAA12230.1; Name=B; Name=A Name=E EMBL; EMBL; EMBL; ----| -[6]
SEQUENCE FROM N.A. (ISOFORM B).
STRAIN-Sprague-Dawley, TISSUE-Spleen;
STRAIN-Sprague-Dawley, TISSUE-Spleen;
Park J.H., Ju S.K., Na S.Y., You K.H., Kim K.L.;
Park J.H., Ju S.K., Na S.Y., You K.H., Kim K.L.;
"Molecular cloning, sequencing, and recombinant expression of the long "Molecular cloning, sequencing, and recombinant expression of the long form of the rat leptin receptor isolated from whole spleen RNA.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. C.T. Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H., Mori K., Tamura N., Hosoda K., Nakao K., "Molecular cloning of rat leptin the Proceptor isoform complementary DNAs -- identification of a missense mutation in Zucker fatty (fa/fa) STRAIN=Sprague-Dawley; MEDLINE=97415825; PubMed=9268737; Chien E.K., Hara M., Rouard M., Yano H., Phillippe M., Polonsky K.S., Bell G.I., STRAIN=Sprague-Dawley, and Zucker fatty;
MBDLINE=96212906; PubMed=8630068;
Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker fatty (fa/fa) rat."; SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.
STRAIN-Sprague-Dawley, and Zucker fatty; TISSUE-Brain;
MEDLINE-96295531; PubMed-8702432;
Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
"Substitution at codon 269 (glutamine --> proline) of the leptin
receptor (OB-R) cDNA is the only mutation found in the Zucker fatty Increase in serum leptin and uterine leptin receptor messenger RNA SEQUENCE FROM N.A. (ISOFORMS A; B AND B), AND VARIANT FA PRO-269. STRAIN=Sprague-Dawley, and Zucker fatty; MEDLINE=96332408; PubMed=8769097; Hey P.J., Caskey "Leptin receptor missense mutation in the fatty Zucker rat."; Nat. Genet. 13:18-19(1996). SEQUENCE FROM N.A. (ISOFORM B). Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S., 囟 [9] SEQUENCE OF 557-802 AND 843-892 FROM N.A. (ISOFORMS C AND SEQUENCE OF 1-123 FROM N.A.
SEQUENCE OF 1-123 FROM N.A.
Morishita T., Hiddaka T., Kuzuyama T., Noguchi T.;
"Analysis of rat leptin receptor gene.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. Carlsson B.; "Carlsson B.; "Carlsson B.; "Carloning of the rat leptin receptor."; Cubmitted (JUN-1996) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. (ISOFORM A), AND VARIANT FA PRO-269 VARIANT FA PRO-269 STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=65368027; PubMed=8772180;
Wang M.-Y., Zhou Y.T., Newgard C.B., Unger R.H.;
"A novel leptin receptor isoform in rat.";
FEBS Lett. 392:87-90(1996). Biochem. Biophys. Res. Commun. 224:597-604(1996) levels during pregnancy in rats."; 3iochem. Biophys. Res. Commun. 237:476-480(1997) STRAIN=Zucker; TISSUE=Hypothalamus; MEDLINE=96241565; PubMed=8673096; Phillips M.S., Liu Q., Hammond H.A., Dugan V., Biochem. Biophys. Res. Commun. 225:75-83(1996) Biochem. Biophys. Res. Commun. 222:19-26(1996) SEQUENCE OF 694-878 FROM N.A. STRAIN=Sprague-Dawley; TISSUE=Pancreas; Ma Z.; [1] SEQUENCE FROM N.A. (ISOFORM B), AND

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOIG-062959-5; Sequence=VSP 001711, VSP 001712; TISSUB SPECIFICITY: ISOform B is expressed in kidney, liver, lung, ovary, spleen and uterus. Increased level in uterus during gestation. Isoform F is expressed at high levels in liver and spleen and less in brain, stomach, kidney, thymus, heart, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transport leptin
receptor (isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothalamus.

The Phosphorylated on two tyrosine residues. Tyr-985 may be the major site of phosphorylation. Phosphorylation on both sites is required for full activity (By similarity).

To Esabs: The fatty (RA) mutation produces profound obesity of early onset caused by hyperplagia, defective nonshivering thermogenesis, and preferential deposition of energy into adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leibel R.L.; "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tisgue.
SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 2.
                                                      SEQUENCE OF 821-894 FROM N.A. (ISOFORM A).
STRAINWHEAR MUNICH; TISSUE-Kidney;
Totsune W., Takahashi K., Mackenzie H.S., Murakami O., Arihara Z.,
Sone M., Satoh F., Mouri T., Brenner B.M., Ito S.;
"Leptin receptor gene expression in rat kidney.";
"Leptin receptor gene expression in rat kidney.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                         VARIANT FA PRO-269.
MEDLINE=96314329; PubMed=8690163;
Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
Kerehaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproduction.

FUNCTION: The short form (isoform A) may act to transport to the cerebrospinal fluid. The putative soluble receptor S) could function as a transport protein.

SUBCELLUAR LOCATION: Type I membrane protein. Except for which could be secreted.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subfamily 2.
-!- SIMILARITY: Contains 3 fibronectin type III domains.
"Identification of a leptin receptor in islet.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q62959-2; Sequence=VSP_001705, VSP_001706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=C;
IsoId=Q62959-3; Sequence=VSP_001707, VSP_001708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=Q62959-4; Sequence=VSP_001709, VSP_001710;
Name=F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q62959-6; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q62959-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U52966; AAC52587.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D84550; BAA12697.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D84551; BAA12698.1
D85557; BAA12830.1
```

```
90 CGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 -IVREAARIVSDTSLLVDSVLP-----GSSYEVQVRSKRLDGS---GVWSDWSLPQLFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 LKD--EATSCSLHRSANNATHATYTCHMDVFH-----FWADDIFSVNITDQSGNYSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 --PMLV----VKPDFPLGLRMEVTDDGNLKISWDSQTKAPF-----PLQYQVKYLENST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 WAVSPRRKLISVDSRSV-SILPLEFRKDSSYELOVRAGFWPGSSYQGTMSEWSDPV1FQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Gaps
R EMBL; AF287268; AAF89300.1; -.

R EMBL; US31426; BAA12231.1; -.

R EMBL; AB011006; BAA2429.1; -.

R EMBL; AF007818; AA865201.1; -.

R EMBL; AF007818; AA865201.1; -.

R EMBL; AF007819; AA865201.1; -.

R EMBL; AF007819; AA862202.1; -.

R InterPro; IPR008957; FW_III-like.

R InterPro; IPR008957; FW_III-like.

R InterPro; IPR008957; FW_III.

R InterPro; IPR003529; Hemtopoptn_L_F2.

R R Pfam; PF00041; fin3; 2.

R PR051TE; PR013529; Hemtopoptn_L_F2.

R PR051TE; PR01352; Hemtopoptn_L_F2.

R PR051TE; PR01352; Hemtopoptn_TI.

R PR051TE; PR01352; Hemtopoptn_L_F2.

R PR051TE; PR051TE; PR051TE;

R PR05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OB-R) (HuB219).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEPR HUMAN STANDARD; PRT; 1165 AA.
PR4837; Q13592; Q13593; Q13594; Q92919; Q92920; Q92921; Q17597; Q13592; Q13593; Q12594; Q92910; Q15910; Q15810; Q15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASNIC (POTENTIAL).
FIBRONECTIN TYPE-111 1.
FIBRONECTIN TYPE-111 2.
FIBRONECTIN TYPE-111 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.00036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 138; DB
30.9%; Pred. No. 0.00
ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 30.9 hes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 Q 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 0 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
BEPR HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
            ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  સ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ጵ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ⋧
```

```
Thompson D.B., Ravussin E., Bennett P.H., Bogardus C., "Structure and sequence variation at the human leptin receptor gene in lean and obese Pima Indians."; "Hum. Mol. Genet. 6:675-679(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]
SEQUENCE FROM N.A. (ISOFORM A).
SEQUENCE 97215244; PubMed-9961609;
Luoh S.-M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
Enoh S.-M., Di Marco F., Levin N., Apencer S.A., Gurney A., de Sauvage F.J.;
"Cloning and characterization of a human leptin receptor using a
Diologically active leptin immunoadhesin.";
J. Mol. Endocrinol. 18:77-85(1997).
                                                                                                                                                                   Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;
Tidentification and expression cloning of a leptin receptor, OB-R.";
Cell 83:1263-1271(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96270489; PubMed-8666155; Consider Y.V., Consider E.S., Williams C.J., Hyde T.M., Caro J.F.; Consider E.L., Williams C.J., Hyde T.M., Caro J.F.; The hypothalamic leptin receptor in humans: identification of incidental sequence polymorphisms and absence of the db/db mouse and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fetal liver;

MEDIINE=5626286; PubMed=8616721;

Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A., Platika D., Snodgrass H.R.;

Platika D., Snodgrass H.R.;

Platika D., Snodgrass H.R.;

Platika D., Snodgrass H.R.;

Platika D., Snodgrass H.R.;

Narova Ia219/OB receptor isoforms: possible role of leptin in hematopoiesis and reproduction.";

Nat. Med. 2:585-589(1996).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITES, DISULFIDE BONDS, AND PARTIAL SEQUENCE MEDLINE=99003211; PubMed=9786864; Haniu M., Arakawa T., Bures E.J., Young Y., Hui J.O., Rohde M.F., Welcher A.A., Foran T.; "Human leptin receptor. Determination of disulfide structure and N-glycosylation sites of the extracellular domain."; J. Biol. Chem. 273:28691-28699(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS ARG-109 AND ARG-223
MEDLINE-97301763; PubMed-9158141;
                                                                                                                                                                                                                                                                                                                                                                                                                               "A role for leptin and its cognate receptor in hematopoiesis."; Curr. Biol. 6:1170-1180(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE SPLICING DUE TO AN ENDOGENOUS RETROVIRUS.
MEDILINE=99128231; PubMed=9929394;
MEDILINE=99128231; PubMed=9929394;
Kapitonov V.V. Jurka J.;
"The long terminal repeat of an endogenous retrovirus induces
alternative splitcing and encodes an additional carboxy-terminal
sequence in the human leptin receptor.";
J. Mol. Evol. 48:248-251(1999).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
TISSUE=Peral liver;
MEDLINE=9639968; PubMed=8805376;
Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.
MEDLINE=97289527; PubMed=9144432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [5] SEQUENCE FROM N.A. (ISOFORMS A; C AND D)
                                                                                                         SEQUENCE FROM N.A. (ISOFORMS B AND E).
                                                                                                                                                MEDLINE=96128129; PubMed=8548812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fa/fa rat mutātions.<sup>n</sup>;
Jiabetes 45:992-994(1996)
                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT ARG-223
                                                                                                                                                                                                                                                                                                                                                                                                           Matthews W.;
```

```
MEDLINE=97318795; PubMed=9175732;
MEDLINE=97318795; PubMed=9175732;
Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,
Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;
Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;
"Leptin receptor gene variation and obesity: lack of association in a white British male population ",
Hum. Mol. Genet. 6:869-876(1997).
-!- FUNCTION: Receptor for obesity factor (leptin). Involved in the regulation of fat metabolism and in a hematopoietic pathway required for normal lymphopoiesis. May play a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATS.

PTW: Phosphorylated on two tyrosine residues. Tyr-986 may be the PTW: Phosphorylation. Phosphorylation on both sites is required for full activity (By similarity).

SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 2.

SIMILARITY: Contains 3 fibronectin type III domains.

SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                             VARIANTS ARG-109; ARG-223 AND ASN-656.
MEDLINE=97431549; PubMed=9287054;
MEDLINE=97431549; PubMed=9287054;
Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,
Sothern M., Udall J.N., Kahle B., Leibel R.L.;
"Exonic and intronic sequence variation in the human leptin receptor
gene (LERR).";
Diabetes 46:1509-1511(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reproduction.
-!- FUNCTION: The short form (isoform A) may act to transport leptin to the cerebrospinal fluid (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein. Except for form B which could be soluble.
                                                                                                                                                                                                                                                                                                           VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
WINDLINES 99075638; PubMed-8960295;
Roth H., Korn T., Rosentranz K., Hinney A., Ziegler A., Kunz J.,
Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
Transmission disequilibrium and sequence variants at the leptin
receptor gene in extremely obese German children and adolescents.";
Hum. Genet. 103:540-546(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pront-Allternative splicing; Named isoforms=5; Name=B; Synonyms=13.2, OBRb; Isold=P48357-1; Sequence=Displayed; Name=A; Synonyms=6.4, HuB219.3; Isold=P48357-2; Sequence=VSP_001689, VSP_001690; Name=C; Synonyms=12.1, OBRa; Isold=P48357-3; Sequence=VSP_001691, VSP_001692; Name=D; Synonyms=HuB219.2; Isold=P48357-4; Sequence=VSP_001693, VSP_001694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=E;
IsoId=P48357-5; Sequence=VSP_001688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>|</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>!</del>
```

```
MIN; 601007; -.

RO; GO:0004888; F:transmembrane receptor activity; TAS.

RO; GO:0007166; P:cell surface receptor linked signal transdu. ..; TAS.

RO; GO:0007175; P:cell surface receptor linked signal transdu. ..; TAS.

RO; GO:0007175; P:cell surface receptor linked signal transdu. ..; TAS.

RO; GO:0007175; P:cell surface receptor linked signal transdu. ..; TAS.

RO; GO:0006112; P:cell surface receptor linke.

RICEPTO; IPR003965; FRIA.

RICEPTO; IPR003965; FRIA.

RICEPTO; IPR003529; Hemitopottn_L.F2.

RICEPTO; IPR007110; IG-like.

REAM; PR001116; IG-like.

RRART; SW00060; FNI; 4.

RROSITE; PS01353; HEMATOPO_REC_L.F2; 1.

RROSITE; PS01353; HEMATOPO_REC_L.F2; 1.

RODSSITE; RECEPTO; Transmembrane; Glycoprotein; Signal;

W POLINCEPPISH: Receptor; Transmembrane; Glycoprotein; Signal;

W POLINCEPPISH: Receptor; Alternative splicing; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 PP--RNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 NCSVHECCE-----CLVPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINMVKPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 PPLGLHMEITDDGNLKISWSSP-----PLVPFPLQYQVKX-SENSTTVIREADKIVSAT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 SCSLHRSAHNATHATYTCHMDVFHFMADD--IFSVNITDQSCNYSQBCGSFLLAESIKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 137; DB 1; Length 1165; 28.0%; Pred. No. 0.00044; Vative 25; Mismatches 68; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILAR HUMAN STANDARD; PRT; 825 AA.,
P24354; Q96P01;
01-MAR-1992 (Rel. 21, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 SRSV-SILPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIPQTQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEPTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 825 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB09673.1; JOINED.
AAB09673.1; JOINED.
AAB09673.1; JOINED.
AAB09673.1; JOINED.
AAC3660.1; -.
                                                                                                                                                                                                                                                                                                             JOINED.
                                                                                                                                                                                                                                                                                  JOINED
                                                                                                                                                                                                                                                                                                                                                                               JOINED,
                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED
                                                                                                                                                                                                                                                        JOINED
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; US9257; AAB09673.1; ORBEL; US9259; AAB09673.1; ORBEL; US9259; AAB09673.1; ORBEL; US9259; AAB09673.1; ORBEL; US9260; AAB09673.1; ORBEL; US9261; AAB09673.1; ORBEL; US9261; AAB09673.1; ORBEL; US9262; AAB09673.1; ORBEL; US2912; AACS0509.1; EMBL; US2913; AACS0510.1; EMBL; US2914; AACS0510.1; EMBL; US2914; AACS0511.1; EMBL; US2914; AACS0511.1; EMSP; P16471; IBP3.
                                                                                            AAB09673.1;
AAB09673.1;
AAB09673.1;
AAB09673.1;
AAB09673.1;
AAB09673.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Conservative
                                                                                                                                                                                                                                                                                                                                                                               AAB09673.1;
                                                                                                                                                                                                                                                                                                             AAB09673.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
1165
839
862
1165
                                                                  AAB07496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
IL4R HUMAN
ID IL4R H
AC P24334,
DT 01-MAR-
DT 15-MAR-
DE INTERIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
      NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Echwald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A., Andersen T., Chung W.K., Leibel R.L., Pedersen O.; "Amino acid variants in the human leptin receptor: lack of association to juvenile onset obesity." Blochem. Blophys. Res. Commun. 233:248-252(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Teoform A expressed in fetal liver and in heartopoletic tissues and choroid plexus. In adults highest expression in heart, liver, small intestine, prostate and ovary. Low level in lung and kidney. Isoform B is highly expressed in hypothalamus.

DOMAIN: The cytoplasmic domain may be essential for intracellular signal transduction by activation of JAK tyrosine kinase and
```

â

us-09-825-561a-6.rsp

and

```
VARIANT ATOPIC ASTHMA VAL-75.
MEDLINE=9828037; PubMed=9620765;
Mitsuyasu H., Izuhara K., Mao X.-Q., Gao P.S., Arinobu Y., Enomoto T.,
Kawai M., Sasaki S., Dake Y., Hamasaki N., Shirakawa T., Hopkin J.M.;
"Ile50Val variant of IL4R alpha upregulates IgB synthesis and
associates with atopic asthma.";
Nat. Genet. 19:119-120(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
MEDLINE=97224413; PubMed=9070874;
Deichmann K., Bardutzky J., Forster J., Heinzmann A., Kuehr J.;
"Common polymorphisms in the coding part of the IL4-receptor gene.";
Biochem. Biophys. Res. Commun. 231:696-697(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Am. J. Respir. Crit. Care Med. 1001342-33117.
[9]
WEMIANTS PRO-503 AND ARG-576.
WEDIINE=9925014; PubMed=10233717;
Kruse S., Japha T., Tedner M., Sparholt S.H., Forster J., Kuehr J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [4]
Security From N.A.
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi
Nickerson D.A.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Noguchi E., Shibasaki M., Arinami T., Takeda K., Yokouchi Y., Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi H.; "No association between atopy/asthma and the Ile50Val polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT ATOPIC ARG-576.

MEDLINES 98041803; PubMed=9392697;
Herahns 96 K.K., Friedrich M.F., Esswein L.A., Thomas M.L.,
Chatila T.A.;
The association of atopy with a gain-of-function mutation in the
alpha subunit of the interleukin-4 receptor.";
New Engl. J. Med. 337:1720-1725(1997).
                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99425270; PubMed=10493829; Kalush F., Brandon R., Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; Michael Genome depplications and other features in 12 Mb of DNA sequence thuman chromosome 16p and 16q"; Genomics 60:295-308(1999).
                                                                                                                                                                              Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V., Gimpel S.D., Din W.S., Grabstein K.H., Widmer M.B., Park L.S., Cosman D., Beckmann M.P., "Human interleukin 4 receptor confers biological responsiveness defines a novel receptor superfamily.";
                                                                                                                                                                                                                                                                                                                                    MEDLINE=91120547; PubMed=2278997;
Galizzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O.,
Kastelein R., Banchereau J., Howard M., Miyajima A.;
"Molecular cloning of a cDNA encoding the human interleukin 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99322293; PubMed=10390422;
                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Peripheral blood;
MEDLINE-90171849; PubMed-2307934;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Int. Immunol. 2:669-675(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAL-75
  antigen).
IL4R OR IL4RA OR 582J2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT ATOPIC ASTHMA
                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [6]
VARIANT ATOPIC
                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.";
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILIRE-2118-2061, PubMed=11285129;
MEDILIRE-2118-2061, PubMed=11285129;
MEDILIRE-2118-2061, Unla J.M., Padilla O., Arman M., Gimferrer I., Suarez B., Lopez de la Iglesia A., Miserachs N., Vives J.; Lopez de la Iglesia A., Miserachs N., Vives J.; Lopez de la Iglesia A., Miserachs N., Vives J.; Lopez de la Iglesia A., Miserachs N., Vives J.; Liste and definition of eight common alleles for human IL4RA exon 11.";

In seque Antigens 57:216-220(2001).

In seque Antigens 57:216-220(2001).

IL4-dependent immune responses.

IL4-dependent immune responses.

IL4-dependent immune responses.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.

ILS-SUBUNIT: Heterodimer of mapha chain and a common gamma chain.
                           receptor alpha
                                                                                                                                                                                                     Ober C., Leavitt S.A., Tealenko A., Howard T.D., Hoki D.M., Daniel R. Newman D.L., Wu X., Parry R., Lester L.A., Solway J., Blumenthal M., King R.A., Xu J., Meyers D.A., Bleecker B.R., Cox N.J.; "Variation in the interleukin 4-receptor alpha gene confers susceptibility to asthma and atopy in ethnically diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21405389; PubMed=11513543; Andrews R.P., Burrell L., Rosa-Rosa L., Cunningham C.M., Brzerinski J.L., Bernstein J.B., Khurana Hershey G.K.; "Analysis of the Ser786Pro interleukin-4 receptor alpha allelic variant in allergic and nonallergic asthma and its functional
                                                                                                                                                                                                                                                                                                                                                                                     VARIANT ATOPIC DERMATITIS ARG-576.

WEDLINE-20269830; PubMed=10809862;

Olso N., Fukai K., Ishii M.;

"Interleukin 4 receptor alpha chain polymorphism Gln551Arg is associated with adult atopic dermatitis in Japan.";

Br. J. Dermatol. 142:1003-1006(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G0:0005887; C:integral to plasma membrane; TAS.
G0:0004913; F:interleukin-4 receptor activity; TAS.
G0:0005057; F:receptor signaling protein activity; TAS.
G0:0006955; P:immune response; TAS.
G0:0007165; P:signal transduction; TAS.
Delchmann K.A.;
"The polymorphisms S503P and Q576R in the interleukin-4
gene are associated with atopy and influence the signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subfamily 4.
DATABASE: NAME=PROW; NOTE=CD guide CD124 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd124.htm".
                                                                                                                                                                                                                                                                                                                                                               J. Hum. Genet. 66:517-526(2000).
                                                                                                                                                                                  PubMed=10677312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consequences.";
Clin. Immunol. 100:298-304(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC004525; AAC23495;;
EMBL; AF421855; AAL12163:1; -.
PIR; A60386; A60386.
                                                                                                     mmunology 96:365-371 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X52425; CAA36672.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; IIAR; 03-MAR-00.
PDB; IIRS; 15-MAY-97.
PDB; IITE; 26-JAN-95.
Genew; HGNC: 6015; IIAR.
MIM; 147781;
                                                                                                                                                    VARIANT ALA-752.
MEDLINE=20143377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT PRO-786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT ILE-579
                                                                               ransduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88888
```

ò

벙

Macaca mulatta (Rhesus macaque)

```
POTENTIAL.

CYTOPLASNIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).

| N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||: : ||: | : | | : 85 VCHL-----LMDDVVSAD-----NYTLDLWAGQQLLWKGSFKFSEHVKPRAPGNLTVHT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCHMDVFHFMADDIFSVNITDQSGNYSQEC-----GSFLLAESIKPAPPFNVTV-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTDYLQTVICILEMWNLHPST----LTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 TFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 CVSDYMSISTC----EWKONGPTNCSTELRLIYOLVF--LLSEAHTC----IPENNGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Gaps
                                                                PROSITE; PS01355; HEMATOPO REC S F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V -> I.

/FTId=VAR_011661.

S -> A (in dbSNP:1805016).

FTIG=VAR_011662.

S -> P (in 1.8% of the population;

dbSNP:1805014).
                                                                                                                         INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 825;
                                                                                                                                                                                                                                                                                                                                                                                                                   /FIId=VAR 011660.
Q -> R (in atopic dermatitis;
dbSNP:1801275).
                                                                                                                                                                                                                                                                                                                   / (in dbSNP:1805011).
/FIId=VAR 011657.
/ FIId=VAR 011657.
/ FIId=VAR 011658.
S -> L (in dbSNP:1805013).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MYEO; Q9MYK9; Q9MYL1; Q9MYL2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
                                                                                                                                                                                                                                                                                                                                                                                          FTIG=VAR 011659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VAR 011663.
9F886DF5612297F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 E-----FRKDSSYELQVRAGPMPGSSYQGTWSEWS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 EPSIRIAASTLKSGISYRARVRAW---AQCYNTTWSEWS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.3%; Score 135.5; DB 1
26.0%; Pred. No. 0.00038;
rative 25; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTIG-VAR_008035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1163 AA
          InterPro; IPR008957; FW_III-like.
InterPro; IPR003961; FW_III.
InterPro; IPR003531; Hemtopoptn_S_FI.
SWART; SM00060; FW3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              825 AA; 89658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.09
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                        400
                                                                                                                                                                                                                                                                                                                                                                              436
                                                                                                                                                                                                                                                                                                                                                                                                         503
                                                                                                                                                                                                                                                                                                                                                                                                                                     576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          752
                                                                                                                                                                                                                                                                                                                                                   431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     786
                                                                                                                        26
22
22
23
25
25
25
20
20
20
20
20
20
20
20
                                                                                                                                                                                                                                                                                                                                                                              436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     786
                                                                                                                                                                                                                                                                                                                      400
                                                                                                                                                                                                                                                                                                                                                   431
                                                                                                                                                                                                                                                                                                                                                                                                         503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEPR MACMU
                                                                                                                                                   TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                        /ARIANT
                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                            /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                         /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
LEPR MACMU
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWISS furstration the Buropean Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afterement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C., "Monkey leptia receptor mRNA: sequence, tissue distribution, and mRNA expression in the adipose tissue of normal, hyperinsulinemic, and type adiabetic rhesus monkeys.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name-A;
Isold=Q9MYL0-2; Sequence=VSP_001695, VSP_001696;
Isold=Q9MYL0-2; Sequence=VSP_001695, VSP_001696;
ISSUE SPECIFICITY: Widely expressed. High expression of isoform B in liver, adipose tissue, hypothalmus and choroid plexus.
-!- DOMAIN: The cytoplasmic domain may be essential for intracellular signal transduction by activation of JAK tyrosine kinase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reproduction.
-!- FUNCTION: The short form (isoform A) may act to transport leptin to the cerebrospinal fluid (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
- Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Phosphorylated on two tyrosine residues. Tyr-984 may be the major site of phosphorylation. Phosphorylation on both sites is required for full activity (By similarity).

SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the
                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A. (ISOFORMS A AND B).
TISSUB-Adipose tissue;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia! Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecine; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE FROW N.A.
Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for obesity factor (leptin). Involved in regulation of fat metabolism and in a hematopoietic pathway regulation of fat metabolism and in a hematopoietic pathway required for normal lymphopoiesis. May play a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interPro; IPR003529; FWHTOPOPTH L F2.
InterPro; IPR003531; Hemtopopth L F2.
InterPro; IPR003531; Hemtopopth S_F1.
Pfam; PR00041; ff13; 2.
SMART; SM00060; FN3; 4.
PROSITE; P801355; HEMATOPO REC L F2; 1.
PROSITE; P801355; HEMATOPO REC S_F1; 1.
PROSITE; P801355; HEMATOPO REC S_F1; 1.
Alternative splicing; Phosphoxylation.
signal; Repeat; SGNAL 1 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subfamily 2. SIMILARITY: Contains 3 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9MYL0-1; Sequence=Displayed;
                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A AND B).
TISSUE-Adipose tissue;
MEDLINE-98408931; PubMed-9738551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF225874; AAF35388.1; --
EMBL; AF225875; AAF33389.1; --
EMBL; AF222806; AAF35387.1; --
EMBL; AF222806; AAF34683.1; --
HSSP; P16471; 1BP3.
InterPro; IPR008956; CRIA.
InterPro; IPR008957; FW III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR008957; FN III-like. IPR003961; FN III.
                                                                                                                                                                                                                                                                      Obes. Res. 6:353-360(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---
```

```
쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                              45 SCSLHRSAHNATHATYTCHMDVFHFMADD--IRSVNITDQSGNYSQECGSFLLAESIKPA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 NCSVHERCE-----CLVPVPTAKINDTLIACLKITSGGVIFQSPIMSVQPINMVKPD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 PP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 PPLGLEMBITDDGNLKISWSSP-----PLVPFPLQYEVKY-SENSTTVIREADKIVSAT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGUNELE FROM: N.A.

MEDLINE=91344784; PubMed=1889461;
Page T.H., Dallman M.J.;
The Molecular cloning of CDNAs for the rat interleukin 2 receptor alpha and beta chain genes: differentially regulated gene activity in response to mitogenic stimulation.";
Tresponse to mitogenic stimulation.";
Tresponse to mitogenic stimulation.";
L. TIMMUNOLY. 12:1313-2138(1991).
- I-TUNCTION: Receptor for interleukin 2. This beta subunit is involved in receptor mediated endocytosis and transduces the mitogenic signals of IL2.
- GUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R exists in 3 different forms: a high affinity dimer, an intermediate affinity monomer (beta chain), and a low affinity forms also associate with a gamma chain.
- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                    -> KIRGFVMLPRLVLNSQAQVIHPPRPPKVLELQ (IN
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
(High affinity IL-2 receptor beta subunit) (CD122).
                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                 FIBRONECTIN TYPE-INI.
FIBRONECTIN TYPE-INI.
FIBRONECTIN TYPE-INI.
BY SIMILARITY.
FYSTE-- FYDIL (in isoform A).
FTTG-SPD 001695.
MISSING (In isoform A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 SRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 SLLVDGILP----GSSYEVQVRGKRLDG---PGIWSDWSTPHVFTTQ 329
                                                                                                                                                                                                                                                                                                                                                                                  Length 1163;
                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 135; DB 1; Length 11.
28.0%; Pred. No. 0.00065; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                    . 2; AAF35387/AAF34683).
6B7B89108F851895 CRC64;
           SXTRACELLULAR (POTENTIAL).
                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                    Missing (In isoform A). /Frid=VSP 001696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   537 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                   1163 AA; 132295 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                            984
                                                                                                                                                                                                                                                        894
                                                                                                                                                                                                                                                                                        1163
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                        895
                                                                                                                                                                                                                                                                                                                     889
                                                                                    DOMAIN
DISULFID
                                                                                                                                                                                           DISULFID
DISULFID
MOD RES
         DOMAIN
TRANSMEM
                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL2B RAT
                                                                                                                                  DISULFID
                                                                                                                                                                              DISULPID
                                                                                                                                                                                                                                                       VAREPLIC
                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                      DOMAIN
                                                                                                                                                                                                                                           MOD RES
                                       OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       မှ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 RRKLISVDSRSVSLLPLEFRK-----DSSYELQVRAGPMPGSSYQGTWSEWSDPV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 CSHLKCFYNSRANVSC---MWS-------PEEALNVTSCHIHAKSDMRHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEA----TSCSLHRSAH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 NKTCELTPVRQASWACNLILGPLPDSQSLTSVDLLSLSVVCWREKGWRRVKTCTFHPFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 IKPAPPFNVTVTF--SGQYNISWR----SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 NAT -----HATYTCHM -----DVFHFMADDIFSVNIT -- DQSGNYSQECGSFLLAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
  Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created):
01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTERVIAN-
POTERVIAN-
INTERLEUKIN-
EXTRACELLUIAR (POTENTIAL).
POTENTIAL.
CYTOPLASNIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60657 MW; 9C744A24F3361968 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 11.2%; Score 134; DB 1;
Local Similarity 23.1%; Pred. No. 0.0003;
Hes 58; Conservative 41; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                               PO REC S F1; 1.
Glycoprotein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AA
                                                                                                                                                                                                                                                                                  Interpro; IPR002996; CRIA.
Interpro; IPR008957; FN III-like.
Interpro; IPR003961; FN III.
Interpro; IPR003511; Hemtopoptn_SF1.
SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEMATOPO_RBC_SF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                          EMBL; M55050; AAA41429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 IFQTQSEELKE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 AFRTRPADPKE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              26
239
267
537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150
537 AA;
SIMILARITY:
Subfamily 4.
                                                                                                                                                                                                                                                                    P14784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYRG MOUSE
P34902;
                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL2RG.
```

```
Gene 130:303-304(1993).
                        SEQUENCE FROM N.A.
        SEQUENCE FROM N.A.
                                 SEQUENCE FROM N.A.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 G---COIOKEDIQLYQTFVVQLQDPQKPQRRAVQKINLQNLVIPRAPENLTLSNLSESOL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 NISWRSDYEDPAFYMLKGK-LQYELQYR-NRGDPWAV----SPRRKLISVDSRSVSLLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 ELRWKSRH-----IKERCLLOYLVOYRSNRDRSWTELIVNHEPRFSLPSVDE---- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PDLVCYTDYLQTVICILEMWN--LHPSTLTLTWQDQYEELKDEAT--SCSLHRSAHNATH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ATYICHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVT--FSGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 133.5; DB 1; Length 369;
Pred. No. 0.00021;
3; Mismatches 94; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 LEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSEE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB2D5AB459077AC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LKRYTFRVRSRYNPICGSSQQ--WSKWSQPVHWGSHTVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 133.0,
25.2%; Pred. No. 0.000°
tive 33; Mismatches
                                                                                                                                                                                                                                                                 AAA39286.1; -. AAB32904.1; -. AAB32904.1; JOINED. AAB32904.1; JOINED. AAB32904.1; JOINED. AAB32904.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                          S75849; AAB32904.1; JOINED.
S75850; AAB32904.1; JOINED.
S75851; AAB32904.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42241 MW;
                                                                                                                                                                                                 EMBL; D13821; BAA02974.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; 149280; 149280.
HSSP; P31785; 11LM.
MGD; MGI:96551; 112rg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X75337; CAA53085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC014720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
TPOR MOUSE
ID TPOR M
                                                                                                                                                                                                                                                                                                                                                                                                                  MBL;
       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N. TISSUB-Salivary gland;

KIAUSDE-21388257; PubMed=12477932;

Strainberg R.L., Feinfold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T. Wax S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Toshiyiki S., Carminci P., Frange C.,

Brownstein M.J. Usdin T.B., Toshiyiki S., Carminci P., Frange C.,

Brownstein M.J., Usdin T.B., Toshiyiki S., Carminci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., McKernan K.J., Malek J.J., Hulyk S.W.,

Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Cheneration and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Lippoll. L. FUNCTION: Common subunit for the receptors for a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBDITT: The gamma chain is common to the ILL2, IL4, IL7, IL21 and probably also the ILL3 receptors.
-!- SUBCELLIAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 5.
                                                                                                                                                                                                                      STRAIN=CBA/CA;
MEDLINE=9391374; PubMed=8378320;
Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
                                                          Sugamura K.;
       SEQUENCE FROM N.A. WEDLINE=9327575; PubMed=8503926; WEDLINE=93277575; PubMed=8503926; Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K. Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K. Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura chain: "Cloning of the mouse interleukin 2 receptor gamma chain: demonstration of functional differences between the mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96341745; PubMed=8750189;
Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirke J.F.,
Dougherty G.J.;
"Molecular mechanisms regulating the hyaluronan binding activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILNE-95104205; PubMed-7805729; Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P., Fischer A., de Saint Basile G.; Fischer A., te Saint Basile G.; The murine interleukin-2 receptor gamma chain gene: organization, chromosomal localization and expression in the adult thymus."; Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BEDLINE-2366191, PubMed-8359699;

Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;

Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;

"Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Subfamily 5. SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                   Biochem. Biophys. Res. Commun. 193:356-363(1993).
                                                                                                                                                                                                                                                                                                                                             IL-2R gamma chain expression.";
Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adhesion protein CD44.";
Neurooncol. 26:231-239(1995).
```

```
4 LVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATYT-- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPR OR OBR.
Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF
                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                  429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEPR PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                g
                                                                                                                                                     ద
                                                                                                                ò
                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstands. Lucypean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-min receptor precursor (TPO-R) (Myeloproliferative leukemia protein) (C-mpl).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Mus.
1011_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ICFW; TISSUE=Fetal liver;
STRAIN=ICFW; TISSUE=Fetal liver;
MEDLINE=9399094; PubMed=8997366;
MEDLINE=9399094; PubMed=897366;
Suyri M., Cosman D., Gisselbrecht S.;
"Characterization of the murine Mpl proto-oncogene, a member of the hematopoietic cytokine receptor family: molecular cloning, chromosomal location and evidence for a function in cell growth."; Oncogene 8:2607-2615(1993).
-!- FUNCTION: Receptor for thrombopoietin. May represent a regulatory molecule specific for ToPo-R-dependent immune responses.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                        "Murine c-mpl: a member of the hematopoietic growth factor receptor superfamily that transduces a proliferative signal.";
EMBO J. 12:2645-2653(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTODLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN REF. 2).
D -> V (IN REF. 2).
P -> PVRTSPAGE (IN REF. 2).
W, 309CP6EAA3724549 CRC64;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=33327753; PubMed=8334987;
Skoda R.C., Seldin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
Leder P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 132.5; DB 1; Length 625; larity 25.0%; Pred. No. 0.0005; Conservative 25; Mismatches 80; Indels 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
THROMBOPOIETIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00060; FN3; 2.
PROSITE; PS01352; HEWATOPO REC_L_F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 222649; CAA80365.1; -
EMBL; 222657; CAA80372.1; -
EMBL; 235377; CAA52031.1; -
FIR; 535317; 535317.
FIR; 537622; 537622.
INSSP, P19235; IRRN.
MGD; MGI:97076; MP1.
InterPro; IRR002996; CRIA.
InterPro; IRR003961; FN III.
InterPro; IRR003961; FN III.
FRAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69817 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
```

14;

Gape

75;

```
428
                                                                                                                                                                                                                                       LEP----SLGARGGT---LELRPRARYSLOLRA-RINGPTYQGPWSAWSPPARVSTGSE 479
320 DPTWEKCEEEEPRPGSOPALVSRCHFKSRNDSVIHIL-----VEVTTAQGAVHSYLGSP 373
                                                                                                                               FILLAESI-KPAPPFNVTVTFSGQYNISWRSDYBDPAFYMLKGKLQYELQYRNRG-DPWAV 150
                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hu X., Dai R., Li N., Wu C.;
"Expression, detection, and partial cloning of porcine leptin receptor
(OBR) gene.";
                                                                                                                                                                                                             151 -SPRRKLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSE
                                                                                                                                                         | : :: | | : | | : | | : | | 374 FWIHQAVLLPTPSLHWREVSSGRLELEWQHQSSWAA----QETCYQLRYTGEGREDWKV
                                                   -----CHM-----DVFHFMADDIFSVNITDQSGNYSQECGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=9722487; PubMed=9069130; Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.; Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.; "The leptin receptor gene (IRPR) maps to porcine chromosome 6."; Mamm. Genome 8:256-226(1997).

-i. FUNCTION: Receptor for obesity factor (leptin). Involved in the regulation of fat metabolism and in a hematopoietic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy B.D.; "Porcine leptin receptor: molecular structure and expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20388825; PubMed=10911396;
Ruiz-Cortes Z.T., Men T., Palin M.-F., Downey B.R., Lacroix D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 109-123 FROM N.A.
MEDLINE-99016721; PubMed-9800339;
Stratil A., Kopecny M., Moser G., Schroffel J. Jr., Cepica S.;
"Hpall and Real PCR-RFUPS within an intron of the porcine leptin
receptor gene (LRRR) and its linkage mapping.";
Anim. Genet. 29:405-406(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lacroix D.A., Gevry N.Y., Ruiz-Cortes Z.T., Murphy B.D.; "Porcine leptin receptor intron 3, partial."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OBR) gene.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matteri R.L., Carroll J.A.;
"Partial cDNA sequence of the porcine leptin receptor.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                         002671; Q95257; Q9MZS2; Q9N1F9; Q3XSN9; 28-FKB-2003 (Rel. 41, Created) 28-FKB-2003 (Rel. 41, Last sequence update) 15-MXR-2004 (Rel. 43, Last annotation update) Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
                                                                                                                                                                                                                                                                                                                                                            1165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 13-159 AND 916-1088 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Reprod. Dev. 56:465-474(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 408-470 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Yorkshire X Meishan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 7-854 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
STATS.

PTM: Phosphorylated on two tyrosine residues. Tyr-986 may be the major site of phosphorylation. Phosphorylation on both sites is required for full activity (By similarity).

SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008957; FN III-like.
InterPro; IPR008957; FN III-like.
InterPro; IPR003529; Hemtopoptn_LF2.
InterPro; IPR003531; Hemtopoptn_SF1.
Promoting FR00041; fn3; 1.
PROMIT: SW00060; FN3; 2.
PROSITE; PS01353; HEMATOPO_REC_LF2; 1.
PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Subfamily 2. SIMILARITY: Contains 3 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.

CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 3.
BY SIMILARITY.
BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
LEPTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF092422; AAC61766.1; --
EMBL; AF184173; AAF66822.1; --
EMBL; AF167719; AAF66822.1; JOINED.
EMBL; AF167719; AAF89633.1; --
EMBL; AF036908; AAB88625.1; --
EMBL; U67739; AAB07892.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ22162; CAA11142.1; -. AJ223163; CAA11143.1; -. U72070; AAC48707.1; -. P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYL
```

```
98 SIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 CSLHRSAHNATHATYTCHM-----DVFHFMADDIFSVNITDQSGNYSQECGSFLLAE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | | ::: | : | : | | | | | ::: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
HOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
TO SYN -> CVV (IN REF. 3) AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 LISVDSRSV-SILPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 SVA -> CVV (IN REF. 3).

69 T -> M (IN REF. 3).

283 E -> I (IN REF. 1).

350 F -> I (IN REF. 3).

362 S -> P (IN REF. 3).

365 K -> E (IN REF. 3).

365 G -> P (IN REF. 3).

365 G -> P (IN REF. 3).

365 K -> E (IN REF. 3).

365 K -> E (IN REF. 3).

367 T -> I (IN REF. 4).

1047 T -> I (IN REF. 4).

4, 132523 MW; 9F02EADDEDC26D21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 129; DB 1; Pred. No. 0.0022; Pred. No. 0.0022; Pred. S6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: March 3, 2004, 12:36:13 Job time: 9.19281 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.2°
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1165 AA;
       CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                           MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                               MOD RES
           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

```
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Appli
Sequence 2, Appli
Sequence 115, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 115, Appli
Sequence 115, Appli
                                                                                           March 3, 2004, 12:38:15; Search time 28.4967 Seconds (without alignments) 1615.322 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2,
Sequence 2,
Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16,
Sequence 97,
Sequence 30,
                                                                                                                                                           US-09-825-561A-6
1195
1 CPDLVCYTDYLQTVICILEM.....SDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-965-313-2
US-09-923-246-115
US-09-923-246-115
US-09-972-218A-2
US-10-295-32-115
US-10-295-32-115
US-10-295-32-115
US-10-295-32-115
US-10-414-186-2
US-10-414-186-2
US-09-825-561A-16
US-09-825-561A-30
US-09-825-561A-30
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-825-561A-6
US-09-941-973-2
                                                                                                                                                                                                                                                                            809742 seqs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*
                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000.00
1000.00
1000.00
1000.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
```

Sequence 97, Appl Sequence 51, Appl Sequence 51, Appl Sequence 21, Appl Sequence 22, Appli Sequence 23, Appli Sequence 25, Appli Sequence 26, Appl Sequence 27, Appl Sequence 31, Appl Sequence 4, Appli Sequence 65, Appl Sequence 10, Appl Sequence 64, Appli Sequence 67, Appli Sequence 97, Appli Sequence 97, Appli Sequence 97, Appli Sequence 91, Appli Sequence	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
14 US-10-295-723-97 14 US-10-243-072-51 14 US-10-243-072-51 14 US-10-264-634-331 14 US-10-264-634-23 14 US-10-264-634-23 14 US-10-264-634-23 14 US-10-264-634-23 15 US-09-825-561A-72 16 US-09-825-561A-72 17 US-09-825-561A-72 18 US-09-825-561A-72 19 US-09-825-561A-72 10 US-09-825-561A-72 10 US-09-825-561A-72 11 US-10-264-634-10 11 US-09-825-561A-72 12 US-09-825-561A-72 13 US-09-825-561A-72 14 US-10-264-634-10 15 US-09-73-234-6 16 US-09-73-234-6 17 US-09-73-234-6 18 US-09-76-846-6 18 US-09-76-846-6 19 US-09-76-846-6	ALIGNMENTS 61A 61A K, Julia E. 194,731 1222,121 222,121 Mismaches
0.0.0 0.	10n US/ 7677A1 7
11111111111111111111111111111111111111	AND THE PROPERTY OF THE PROPER
11111000000000000000000000000000000000	RESULT 1 US-09-825-561P Sequence 6, Patent No. U GENERAL INF APPLICANT: APPLI

TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLARSIKPAPPFNVTVTFSGQYNISWR 120 TCHMDVFHFWADDIRSVNITDQSGNYSQECGSFLLAESIKPAPPRNYTVTFSGQYNISWR 120 ö

60

```
80 TCHMDVFHFWADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                        121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                        140 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TCHMDVFHFMADDIRSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 TCHMDVFHFMADDIFSVNITDQSGNYSQBCGSFLLAASIKPAPPFNVTVTFSGQYNLSWR.139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SDYEDPAFYMLKGKLQYBLQYRNRGDPWAVSPRRKLISVDSRSVSLLPLBFRKDSSYBLQ 180
                                                                                                                                                                                             61 TCHMDVFHFMADDIPSVNITDQSGNYSQECGSFLLARSIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140.SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSYSLLPLBFRKDSSYBLQ.199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 CPDLVCYTDYLQTVICILENMANLHPSTLTLTMQDQYEELKOEATSCSLHRSAHNATHATY 79
                                                                                                                                  20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sprecher, Cindy A. APPLICANT: Sprecher, Cindy A. APPLICANT: Foster, Cindy A. APPLICANT: Foster, Cindy A. APPLICANT: Foster, Donald C. APPLICANT: Holly, Richard D. APPLICANT: Gross, Jane A. APPLICANT: Johnston, Janet V. APPLICANT: Johnston, Janet V. APPLICANT: Johnston, Janet V. APPLICANT: Hammond, Angela K. TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT APPLICATION NUMBER: EARLIER PRILING DATE: 2000-03-09
PRIOR APPLICANTON NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR PILING DATE: BARLIER FILING DATE: 1999-03-11
PRIOR PILING DATE: BARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastesQ for Windows Version 3.0
LENGTH: 538
LENGTH: 538
FUND 115
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPDLVCYTDYLQTVICILEMMNLHPSTLTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1195; DB 9; Length 538; 100.0%; Pred No. 2:4e-117; tive 0; Mismatches 0; Indels 0;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                   181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
  100.0%; Pred. No. 2.4e-117; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 115, Application US/09923246
No. US20020128446A1
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%;
Matches 218; Conservative
Best Local Similarity 100. Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-923-246-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                               요
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09965313
; Fatent No. US2002009680A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: and Uses Thereof
; TITLE OF INVENTION: and Uses Thereof
; TITLE OF INVENTION: and Uses Thereof
; TITLE OF INVENTION: US/09/965,313
; CURRENT APPLICATION NUMBER: US/09/965,313
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/313,913
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 8
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT

CORCANISM: Home sapiens IL-2/IL-9 Receptor Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 SDYEDPAFYMLKGKLQYELQYENQYENGDPWANSPRRKLISVDSRSNSLLPLEFRKDSSYELQ 199
                                SDYEDPAFYMLKGKLOYELOYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYBLO 180
                                                                                121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1195; DB 9; Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 1195; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 1e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VRAGPMPGSSYOGTWSEWSDPVIFOTOSEELKEGWNPH 218
                                                                                                                                        181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                           181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEBLKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL ORPHAN RECEPTORS
TITLE OF INVENTION: NOVEL ORPHAN RECEPTORS
FILE REFERENCE: REGGSO
CURRENT APPLICATION NUMBER: US/09/128,820
FRIOR APPLICATION NUMBER: US/09/128,820
FRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09941973
Patent No. US20020160451A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-941-973-2
                                                                                                                                                                                                                                                                                                           US-09-941-973-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-965-313-2
                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                   ઠે
                                                                             셤
                                                                                                                                        ઠ
                                                                                                                                                                                                음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
```

us-09-825-561a-6.rapb

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSSYSLQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTMQDQYEELKDBATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09972218A
Sequence 2, Application US/09972218A
Sequence 2, Application US_09972218A
Sequence 2, Application Wo. US20030049798A1
GENERAL INFORMATION:
APPLICANT: Carter, Laura
APPLICANT: Whiteers, Matthew J
APPLICANT: Voung, Deborah A.
APPLICANT: Collins, Mary
APPLICANT: Dowe, Leslie D.
APPLICANT: Dowe, Leslie D.
APPLICANT: Unger, Michelle
TITLE OF INVENTION WULL IS 000,0972,218A
CURRENT ELLING DATE: 2008-552CIP2
CURRENT APPLICATION NUMBER: 09/569384 <---
CURRENT PILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/560766
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 21
NUMBER OF SEQ ID NOS: 21
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 538;
                                                                      APPLICANT: Sprencher, Cindy A. APPLICANT: Sprencher, Cindy A. APPLICANT: No. US20020137677A1ak, Julia E. APPLICANT: West, James W. APPLICANT: West, James W. APPLICANT: Prest, James W. APPLICANT: Prest, James W. APPLICANT: Holly, Richard D. APPLICANT: Holly, Richard D. APPLICANT: Nelson, Andrew J. TITLE OF INVENTION: SOUUREZ ALPHAII CYTCKINE RECEPTORS FILE REFERENCE: 00-22 COUTAND NUMBER: US 60/194,731
PRIOR PPLICATION NUMBER: US 60/194,731
PRIOR PLILING DATE: 2000-04-05
PRIOR PLILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 2: SEQ ID NOS: 86
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1195; DB 9; Best Local Similarity 100.0%; Pred. No. 2.4e-117; Matches 218; Conservative 0; Mismatches 0;
Sequence 2, Application US/09825561A Patent No. US20020137677A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-561A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
USEQUENCE 2. Application US/10264634

| Sequence 2. Application US/10264634
| Publication No. US20030108549A1
| Sequence 2. Application No. US20030108549A1
| GENERAL INFORMATION:
| APPLICANT: Donaldaon, Debra et al.
| TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor A FILE REFERENCE: G15320-P3
| CURRENT APPLICATION NUMBER: US/10/264,634
| CURRENT PILING DATE: 2000-10-4
| PRIOR PLILOR DATE: 2000-04-28
| PRIOR PELICATION NUMBER: 09/560,766
| PRIOR PELICATION NUMBER: 09/560,766
| PRIOR PELICATION NUMBER: 09/569,384
| PRIOR PLILOR DATE: 2000-05-11
| PRIOR PELICATION NUMBER: 60/972,218
| PRIOR PLILOR DATE: 2001-00-04
| PRIOR PLILOR DATE: 2001-04-04
| PRIOR PLILOR DATE: 2001-04-17
| NUMBER: PRIOR PLILOR DATE: 2001-04-17
| SPIOR DATE: PATENTIAL DATE: 2001-04-17
| SPIOR PLILOR DATE: 2001-04-17
| SPIOR PLILOR DATE: 2001-04-17
| SPIOR PLILOR DATE: 2001-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 SDYEDPARYMLKGKTLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                            61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                              80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLARSIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                   20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDBATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                          1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1195; DB 14; Length 538; llarity 100.0%; Pred. No. 2.4e-117; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                      Query Match 100.0%; Score 1195; DB 10; Length 538; Best Local Similarity 100.0%; Pred. No. 2.4e-117; Matches 218; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                            LENGTH: 538
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Human
US-10-264-634-2
                                                                                              ; OKGANISM: DU.
US-09-972-218A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
; SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

```
61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 TCHMDVFHFMADDIFSVNITDOSGNYSOECGSFLLAESIKPAPPFNVTVTFSGOYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 CPDLVCYTDYLQTVICILEMMNLHPSTLTLTWQDQYEELKOBATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1195; DB 14; Length 538; 100.0%; Pred. No. 2.4e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                        APPLICANT: NO. 92002232AAAAA, ULITA B.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Foreter, Clindy A.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Melson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Mammond, Angela R.
TITLE OP INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND FILE REFERENCE: 99-16
CURRENT PILLING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR PILLING DATE: 1999-03-09
PRIOR PILLING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR PILLING DATE: 1999-03-11
PRIOR PILLING DATE: 1999-03-11
PRIOR PILLING DATE: 1999-07-01
NUMBER OF SEO ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 VRAGPMPGSSYQCTWSEWSDPVIFQTQSEELKEGWNPH 237
200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. US20030134390Alak, Julia E.
TITLE OF INVENTION: ZALPHALL LIGAND ANTAGONISTS
FILE REPERENCE: 01-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                       APPLICANT: No. US20030125524A1ak, Julia E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
                                                                                                          -10-295-723-115
Sequence 115, Application US/10295723
Publication No. US20030125524A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/10282622 Publication No. US20030134390A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-282-622-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 TCHMUVFHFWADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVIVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SDYSDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYSELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                  20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                 1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                         Query Match 100.0%; Score 1195; DB 14; Length 538; Best Local Similarity 100.0%; Pred. No. 2.4e-117; Matches 218; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1195; DB 14; Length 538; Best Local Similarity 100.0%; Pred. No. 2.4e-117; Matches 218; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. US203030148447Aiak, Julia E.
APPLICANT: Hammond, Angela K.
TITILR OF INVENTION: CYTOKINE RECEPTOR ZAPLHALI
FILE REPRENCE: 98 -55C1
CURRENT APPLICATION NUMBER: US/10/243,072
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR PILING DATE: 1998-09-23
PRIOR FILING DATE: 1999-03-09
PRIOR PRIOR POSE: 1999-03-09
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-03-03
NUMBER: OF SEQ ID NOS: 92
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LEWGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10243072
Publication No. US20030148447A1
                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-282-622-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-243-072-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-243-072-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

```
Query Match 100.0%; Best Local Similarity 100.0%; Matches 218; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-456-780-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-825-561A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-825-561A-16
                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
                                                                                                                                                                                                                                                                                                                                                        ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 SDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKIJSVDSRSVSLLPLBFRKDSSYELQ 199
140 SDYEDPAFYMLKGKLQYELQYRURGDPMAVSPRRKLISVDSRSVSLLPLEFRKDSSYSLQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/404,641

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: EARLIER PILING DATE: 1998-09-23

PRIOR PILING DATE: EARLIER FILING DATE: 1998-09-23

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06

SUFTAME: PASISEQ for Windows Version 3.0

LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10456780;
Publication No. US20040009150A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nelson, Andrew J.
APPLICANT: Hughes, Steven D.
TITLE OF INVENTION: USE OF IL.21 IN CANCER AND
TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR FILING DATE: 2002-06-07
                                                                  181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1195; DB 14; Best Local Similarity 100.0%; Pred. No. 2.4e-117; Matches 218; Conservative 0; Mismatches 0;
                                                                                                            200 VRAGPMPGSSYQGTWSEWSDPVIFOTOSEELKEGWNPH
                                                                                                                                                                                                                  Sequence 2, Application US/10414186
Publication No. US20030175825A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. US20030175825A1ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/10/414,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-10-414-186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-456-780-6
                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ?
                                                               ਨੇ
                                                                                                          용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ጵ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDYEDPAPYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 SDYEDPAFYMLKGKLQYELQYENRGDPWAVSPRRKLISVDSKSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBBLKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFSGOYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                DB 15; Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1195; DB 9; Length 567; Best Local Similarity 100.0%; Pred. No. 2.6e-117; Matches 218; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: No. US2002013767Alak, Julia E.
APPLICANT: West, James W.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Hollon, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHAII CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR PLILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SSQ ID NO 16
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: soluble zalphallR/IgGgammal polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRAGPMPGSSYQGTWSEWSDPVIFOTOSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                      2.4e-117;
                                                                                                                                                                                                                                                                100.0%; Score 1195; 100.0%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sprecher, Cindy A. APPLICANT: No. US20020137677Alak, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09825561A Patent No. US20020137677A1 GENERAL INFORMATION:
```

```
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDYEDPAFYMLKGKLOYELOYKNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSSYELO 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: MBP-zalphall soluble receptor polypeptide sequence
US-09-923-246-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASISEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                          200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1195; DB 9;
100.0%; Pred. No. 2.8e-117;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hamond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REPRENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                       Application US/09923246
20020128446A1
                                                                                                                                                                                                                                              APPLICANT: No. US20020128446Alak,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                        Gross, Jane A.
Johnston, Janet V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509
ò
                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
```

APPLICANT: Sprecher, Cindy A. APPLICANT: No. US20020137677A1ak, Julia E. APPLICANT: West, James W.

West, James W. Presnell, Scott R. Holly, Richard D. Nelson, Andrew J.

> APPLICANT: APPLICANT: APPLICANT:

Sequence 30, Application US/09825561A Patent No. US20020137677A1 GENERAL INFORMATION:

```
389 CPDLVCYTDYLOTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAENATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLABSIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: MBP-human zalphall soluble receptor fusion CTHER INFORMATION: polypeptide US-09-825-561A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1195; DB 9;
100.0%; Pred. No. 2.8e-117;
tive 0; Mismatches 0;
                                              CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: March 3, 2004, 12:50:51
Job time : 28.4967 secs
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 218; Conservative
```

Human Human

ABR61411
ABR61415
ABR61415
AAR61415
AAX69890
AAX69890
AAX69890
AAX69890
AAX69890
AAX69890
AAX69890
AAX69890
AAX6983742
AAX697337

Human Human

Human Human

Mouse Human

Human

Human Human

		-	56	1187
	GenCore version 5.1.6		27	1180
	Copyright (c) 1993 - 2004 Compugen Ltd.		28	1180
•			58	1180
			30	1180
OM protein - pro	OM protein - protein search, using sw model		31	1180
			32	1180
Run on:	March 3, 2004, 12:24:04; Search time 52.0065 Seconds		33	1170
	(without alignments)		34	1159
	1184.377 Million cell updates/sec		32	1145
			36	1138
Title:	US-09-825-561A-6		37	1112
Perfect score:	1195		38	1077
Sequence:	1 CPDLVCYTDYLQTVICILEMSDPVIFQTQSEELKEGWNPH 218		39	1077
			40	1077
Scoring table:	BLOSUM62		41	1077
	Gapop 10.0 , Gapext 0.5		42	1077
			43	844
Searched:	1586107 seqs, 282547505 residues		44	844
			45	844
Total number of	Total number of hits satisfying chosen parameters: 1586107			
Minimum DB seg 1	ength: 0			
Maximum DB seq 1	Maximum DB seq length: 2000000000			

Match 0% Match 100% first 45 summaries

Minimum M Maximum M Listing f

Post-processing:

05-APR-2000; 2000US-0194731P. 28-JUL-2000; 2000US-0222121P.

(ZYMO) ZYMOGENETICS INC.

Nelson AJ; Presnell SR, Holly RD, Sprecher CA, Novak JE, West JW,

n.

Human sol Human hae Human MU-A buman z HUMAN Orp Human cyt Human IG4 Human IG4 Human IG4 Human Sol Human Sol Human Sol Human MU-Human int Human int Human MI-Human int Human MI-Human int Human MI-Human int Human Cyt
AAY79312 AAB48001 ABB81960 AAU11912 AAE13726 AAU11978 ABR61402

AAE14939 ABU62888

AAB18629 AAY79316

AAE13733

Aay46029 Aay46029 Aay46029 Aay46029 Aay201450 Aay201450 Aay201450 Aay20161 Aay20161 Aay20161 Aay20161 Aay20161 Aay20161 Aay20191 Aay201919 Aay201919 Aay201919 Aay201919 Aay201919 Aay201919 Aay201919 Aay201919 Aay201919

Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune response in a mammal.

Claim 27; Page 176-178; 243pp; English:

The invention relates to an isolated soluble zalphall cytokine receptor polypeptide and their cDNA molecules. Zalpha proteins are useful for inhibiting or antagonising the ligand activity-induced proliferation of haematopotetic cells man haematopotetic cells progenitors preferably lymphoid cells which are natural killer cells or cytotoxic T cells. Zalpha is useful for treating immume and inflammatory disorders, for reducing proliferation of neoplastic B.or T cells, for suppressing an

Human Zal Human HNO Human HNO

AAY94304 AAU08728

ABW00884

Human, Zalphall, cytokine receptor, immunosuppressive, cytostatic; inflammatory disorder, haemostatic; cell proliferation; immune disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; myasthenia gravis; systemic lupus erythematosus; SLB; diabetes; asthma; ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis; viral infection. Human soluble Zalphall cytokine receptor protein fragment AAE13728 standard; protein; 218 AA (first entry) 26-FEB-2002 AAE13728; Homo RESULT 1

WO200177171-A2.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseq11990s:* geneseq72001s:* geneseq72001s:* geneseq72002s:* geneseq72003bs:* geneseq72003bs:*

geneseqp1980s:*

Database

SUMMARIES

DB

% Query Match Length D

Score

18-OCT-2001

03-APR-2001; 2001WO-US010872

Human Human Human Human

Description

WPI; 2002-025898/03. N-PSDB; AAD22920.

N

```
AAY69883
ID AAY6
셤
                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                            ö
                                                                                                                                                                                                                  TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                        TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                         121 SDYEDPAFYMLKGKLOYELOYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKOSSYELO 180
                                                                                                                                                                   9
                                                                                                                                                                                          9
         useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes; asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, sepsis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble Zalphall cytokine receptor protein fragment
Zalpha is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, Orphan Cytokine Receptor-10, OCR10, chromosome 16p12, cytokine, screen, cognate ligand, treatment, endocrine disorder, immune disorder.
                                                                                                                                                                                  CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                  CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                             Gaps
                                                                                                                                            ó
to an antigen or pathogen.
                                                                                                                   Length 218;
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN Orphan Cytokine Receptor-10 (OCR10) polypeptide
                                                                                                                                                                                                                                                                                                                                 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proline_hinge_motif_region
                                                                                                                 Score 1195; DB 5;
Pred. No. 4.3e-115;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238. .255
/label= Transmembrane domain
/note= "Putative and hydrophobic"
                                                                                                                                                                                                                                                                                                                 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proline_hinge_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Jak-binding_region
'note= "Potential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mature_HUMAN_OCR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morris J, Valenzuela DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .21
|abel= Signal_peptide
response in a mammal exposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   AAY45029 standard; protein; 289 AA
                                                                                                                                            ő
                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US016060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00128820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .169
| label= P-
|2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122. .123
/label= Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263. .278
/label= Ja
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. .289
label= M
                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 218; Conservative
                                                                                             Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masiakowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WC200008152-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000
                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                           AAY45029;
                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
AAY45029
88888888888
                                                                                                                                                                      ò
                                                                                                                                                                                          g
                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                       셤
```

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 SDYEDPAFYMLKGKLQYELQYENGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                           for
                                                                                                                                                                                                                                                             The present sequence is the HUMAN Orphan Cytokine Receptor-10 (OCR10) polypeptide. HUMAN OCR10 gene is located on chromosome 16pl2. It is expressed at high levels in spleen, thymus, peripheral blood leucocytes and lymph nodes and moderately in heart and placenta. It has a role in immune system and cytokine function. It is useful in screening for cognate ligands or drugs that mediate survival and differentiation of cells expressing this receptor. Modified HUMAN OCR10 or its agonist can be used in the treatment of endocrine or immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CPDLVCYTDYLQTVICILEMMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                           screening
                                                                     New HUMAN orphan cytokine receptors 10 and 10-A useful for screenir drugs e.g. receptor agonists that may mediate survival and differentiation in cells naturally expressing the receptor and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human haemopoietin receptor family member NR8alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1195; DB 3;
100.0%; Pred. No. 6.4e-115;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                 Example 1, Page 21; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY69883 standard; protein; 361
                                                                                                                                                          screening for cognate ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-JP003351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-00214720
98JP-00297409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-116933/10
N-PSDB; AAZ59237.
WPI; 2000-205707/18.
N-PSDB; AAZ50746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maeda M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ношо варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9967290-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1998;
19-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nomura H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY69883
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be
                                                                                                                                                                                                                                                                                                                                                                                                                                SDYEDPAFYMLKGKLOYELOYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELO 199
                                                                                                                                                                                                                                                                                                                                     TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                    TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                    SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                     79
                                                                                        This sequence represents a novel haemopoietin receptor protein family NR8, designated NR81lpha. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid encoding the MU-1 hematopoietin receptor protein, used treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.
                                                                                                                                                                                                                                                                      1 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYBELKDBATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                         CPDLVCYTDYLQTVICILIEMWNLHPSTLTLTWQDQYBELKDBATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                           Gape
             receptor protein family NR8 used for diagnosis of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This represents a MU-1 hematopoietin receptor protein. The protein produced by standard recombinant methodology. The MU-1 protein has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy; cell proliferation; cytokine production; immune response; cancer; autoimmune disease; transplant rejection; hematopoiesis; anemia; gene mapping; nutritional supplement; human.
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                          Length 361;
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237
                                                                                                                                                                                                         Query Match
100.0%; Score 1195; DB 3;
Best Local Similarity 100.0%; Pred. No. 8.9e-115;
Matches 218; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRAGPMPGSSYQGTWSEWSDPVI POTOSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MU-1 hematopoietin receptor protein.
                                                             Claim 1; Fig 5-6; 176pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY27450 standard; protein; 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US005854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00040005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ungar M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-562115/47.
N-PSDB; AAZ07535.
               Hemopoietin receptor
Formation disorders.
                                                                                                                                                                            Sequence 361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donaldson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
ઠે
                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                     ठ
                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

```
biological activity of the MU-1 hematopoietin receptor superfamily chain.

It,is used to screen for specific binding agents; to raise specific antibodies; as assay reagants, tissue markers etc. and therappeutically optionally expressed from the MU-1 gene by gene therapy). Many possible activities/uses of the MU-1 protein are described without supporting evidence, e.g. they regulate cell proliferation and differentiation, induce production of cytokines, simulate or suppress an immune response (e.g. for treating immune deficiency of any etiology, cancer or autoimmune disease, and for preventing transplant rejection) and response to hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a research reagent, for recombinant production of the protein, as tissue or molecular weight marker, for gene mapping; for production of anti-DNA or anti-protein antibodies etc. The MU-1 protein and the nucleic acids are also useful as nutritional supplements or sources and the antibodies can be used therapeutically, as assay reagents and for affinity purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDYEDPAFYMLKGKLOYELOYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 SDYEDPAFYMLKGKLQYELQYENRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell proliferation; lymphoma; B cell tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human cytokine, designated zalphall ligand, useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCHMDVFHFMADDIFSVNITDQSGNYSQECGFFLARSIKPAPPFNVTVFFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                   20 CPDLVCYTDYLQTVICILEMWNTHPSTLTLTMQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                   CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                            Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foster DC, Holly RD;
Dillon SR, Hammond AK;
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRAGPMPGSSYQGTWSEWSDPVIPQTQSEBLKEGWNPH 218
                                                                                                                                                                                                                                                                                                                            100.0%; Score 1195; DB 2;
100.0%; Pred.No. 1.6e-114;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zalphall ligand; cytokine; haematopoietic tumourigenesis; leukaemia; hematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human zalphall ligand polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sprecher CA,
Nelson AJ, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00265992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18634 standard; protein; 538 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2000; 2000WO-US006067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00264908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novak JE, Presnell SR, Gross JA, Johnston JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-565600/52.
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA75557
                                                                                                                                                                                                                                                                                              Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200053761-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                               Best Local Simi
Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB18634;
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
```

N-PSDB; AAZ50748.

```
The present sequence represents a human zalphall ligand polypeptide, which is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of haematopoletric cells in vitro and in vivo. Zalphall ligand polymucleotides can be used as primers or probes for cloning the zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against calphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regularing hematopolesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polymucleotides, antagonists, agonists and antiboddes are also useful for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDYEDPAFYMLKGKLOYELLOYRNRGDPWAVSPRRKLISVDSRSVSLLPLFRKKDSSYELO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
the proliferation and/or development of hematopoietic cells in vitro and in vivo, and for treating tumorigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, Orphan Cytokine Receptor 10-A; OCR10-A; cytokine; screen; cognate ligand; treatment; endocrine disorder; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN Orphan Cytokine Receptor 10 (OCR10)-A polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1195;
100.0%; Pred. No. 1.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masiakowski PJ, Morris J, Valenzuela DM;
                                                         Disclosure; Page 255-256; 256pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY45031 standard; protein; 538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US016060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-205707/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200008152-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY4503
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYSLQ 199
                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                           79
                             New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for drugs e.g. receptor agonists that may mediate survival and differentiation in cells naturally expressing the receptor and for
                                                                                                                                       The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus, peripheral blood leucocytes and lymph ndes and moderately in heart and placenta. It has a role in immune system and cytokine function. It is useful in screening for cognate ligands or drugs that mediate survival and differentiation of cells expressing this receptor. Modified HUMAN OCR10-A or its agonist can be used in the treatment of endocrine or immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                           20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLABSIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                             1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hemopoietin receptor protein family NR8 used for diagnosis of blood
                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                            100.0%; Score 1195; DB 3; Length 538; 100.0%; Pred. No. 1.6e-114; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemopoietin receptor family; NRB; antibody; diagnosis; blood formation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human haemopoietin receptor family member NR8gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                Example 10; Page 39-41; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY69886 standard; protein; 538 AA.
                                                                                screening for cognate ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-00214720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-JP003351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-116933/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maeda M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ59240
                                                                                                                                                                                                                                                                                                Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1998;
19-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9967290-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nomura H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69886;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
#X#####XXX00000000XX
                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

ö

Gaps

ö

0; Indels

Length 538;

5; DB 3; 1.6e-114;

9 79

```
ö
                                                                                                                                                                                                                                                                                                                                                              SDYEDPAFYMLKGKUQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "cytokine-binding domain; a polypeptide comprising
this domain is specifically claimed in Claim 27(a)"
                                                                                                                                                                                                                                                                                 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                           TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                        SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                     This sequence represents a novel haemopoietin receptor protein family NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders
                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "intracellular signalling domain, a polypeptide comprising this domain is specifically claimed in Claim 27(6)"
                                                                                                                                                                                                                                           CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDBATSCSLHRSAHNATHATY
                                                                                                                                                                                                                     1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "mature protein; a polypeptide comprising the mature protein is specifically claimed in Claim 27(d) 20. .237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal transduction; growth factor; cancer; tumour; infection; immunosuppressive; immunostimulant; autoimmune disease; leukaemia; lymphoma; transplant rejection; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 16p11.1; apoptosis;
                                                                                                                                                                                          ó
                                                                                                                                                              Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                   VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                      VRAGPMPGSSYQGTWSEWSDPVIPQTQSEELKEGWNPH 237
                                                                                                                                                             100.0%; Score 1195; DB 3; 100.0%; Pred. No. 1.6e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "penultimate strand region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Box II signalling site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267. .273
/note= "Box I signalling site"
301. .304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane domain"
                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .19
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              penultimate , 214. .218 /note= "WGXWS motif" 238. .255 /note= "tro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine receptor; zalphall; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                             Claim 4; Fig 9-10; 176pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY79312 standard; protein; 538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytokine receptor zalphall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                           Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301. .3
/note=
formation disorders.
                                                                                                                                Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2000
                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY79312;
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
ઠ
                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                         à
```

```
The present sequence is that of zalphall, a novel human class I cytokine receptor that may be involved in an apoptotic cellular pathway, or is a cell-cell signalling molecule, growth factor receptor, or extracellular cells. Signalling molecule, growth factor hormone activity. The sequence was deduced from a cDNA clone (see AAZ94533) isolated from a sequence was deduced from a cDNA clone (see AAZ94533) isolated from a cord library. Polypeptides comprishing amino acids 20-237, 20-255, 25-538, 20-538 and 1-538 of the present sequence are claimed. Zaphall cord library. Phen bush is supplement in the Raji cell line (ATC CCL 86) derived from Burkitt's lymphona. Zalphall polypeptides, and fusion cordinate the marks is also abundant in the Raji cell line (ATC CCL 86) derived from Burkitt's lymphona. Zalphall polypeptides, and fusion cordinates including them, can be obtained by expression in recombinant consecuence in the are used; to detect ligands and falso ligand agonists and antagonists) that stimulate proliferation and/or development of areplacement for serum in culture media; in vitro or in vivo, e.g. as a replacement for serum in culture media; in vitro or in vivo, e.g. as cortivity (direct antagonists) and for purification of cognate ligands activity of vaccines, suppressing tumours, treating leukopenia and crivity of vaccines, suppressing tumours, treating leukopenia and improving T-cell regeneration after bone marrow transplant rejection and to treat T-cell leukemia or lymphoma or prevent transplant rejection and to treat T-cell leukemia or lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCHMDVFHFMADDIPSVNITDQSGNYSQECGSFLLARSIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid encoding zalphall polypeptide, useful for treating e.g. viral infection or tumors, and for identifying ligands that stimulate cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 TCHMDVFHFMADDIFSVNITDQSGNYSQBCGSFLLABSIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1195; DB 3;
100.0%; Pred. No. 1.6e-114;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                         Hammond AK;
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27(e); Page 148-149; 190pp; English.
                                                                                                                                                                                                                                       Novak JE,
                                                                                                                98US-00159254.
99US-00265117.
99US-00347930.
                                                                            99WO-US022149.
                                                                                                                                                                                                                                                                              WPI; 2000-292825/25.
N-PSDB; AAZ94533, AAZ94534.
                                                                                                                                                                                                                                       Conklin DC,
                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 538 AA;
WO200017235-A2
                                                                                                                                                                                                                                     Presnell SR,
                                                                                                                                     09-MAR-1999;
06-JUL-1999;
                                                                            23-SEP-1999;
                                                                                                                    23-SEP-1998;
                                    30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

ö

9 79 139

RESULT 9

us-09-825-561a-6.rag

Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory; T-lymphocyte-related disorder; antiarthritic; antipsoriatic; human; immunosuppressive; antiasthmatic; antiallergic; antithyroid; cytostatic; antidiarrheic; nephrotropic; gene therapy. el interleukin-9/interleukin-2 receptor-like polypeptides useful for gnosis and treatment immune, inflammatory and respiratory disorders in screening assays for identifying modulators. Human IL-9/IL-2 receptor-like 16445 protein. 1. .19 /note= "signal peptide" "mature protein" Claim 8; Page 104-106; 119pp; English Location/Qualifiers Ą. protein; 538 18-MAY-2000; 2000WO-US013687 99US-00313913 (MILL-) MILLENNIUM PHARM INC (first entry) .538 /note= 2001-016209/02. standard; N-PSDB; AAC84147. 40200069880-A1 18-MAY-1999; 19-MAR-2001 Homo sapiens 23-NOV-2000 diagnosis AAB48001; Hodge MR; Peptide Protein Novel

The invention relates to isolated human and murine interleukin-9 (IL-9) (IL-2 receptor-like polypeptides. The plasmid containing the encoding CDMA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like polypeptides (16445 proteins) can be recombinantly produced using standard recombinant methodology. The 16445 proteins are used for identifying their modulators and for diagnosis and treatment of immune, inflammatory and respiratory disorders and disorders associated with lungs, colon, kidney and lymphoid tissues including atopic conditions particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic inflammatory diseases and graft verses host disease, disorders involving the colon such as diarrhoea, dysentery, infectious entercolitis, kidney disorders including polycystic kidney disease, cystic renal dysplasia, carcinoids. The 16445 polypeptides are also useful as modulating agents in cellular processes including growth promoting activity, particularly che detection of IL-9/IL-2 receptor-like encoding nucleic acid is useful as primers or hybridization probes for the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for tissue typing and in forensic biology. The present sequence represents the human IL-9/IL-2 receptor-like polypeptide (AAH16445)

Sequence 538 AA;

The invention relates to isolated interleukin (IL)-9/IL-2 receptor-like polypeptide, 16445. The 16445 polypeptides can be expressed by standard recombinant methodology. The 16445 polypeptides can be expressed by standard recombinant methodology. The 16445 polypeptides can be expressed by standard recombinant methodology. The 16445 polypeptides particularly for the treatment of immune and respiratory disorders, particularly for the treatment of immune and respiratory disorders, including allergic conditions, such as asthma and allergy, including allergic rhinitis, psoriasis, the effects of pathogen infection, chronic inflammatory disease. Organ sepecific autoimmunity, graft rejection, and graft versus host disease. The molecules are also useful as modularing agence in a variety of callular processes including growth promoting activity, particularly the antigen contain haemopoletic progenitors, inman T cells, because inflammatory, and thymnic lymphomas and neuronal cell lines. They are useful for the modulation, diagnosis, and treatment of immune, inflammatory, and respiratory disorders and disorders associated with lungs, colon, kidney, and lymphoid tissues including tonsil and thymnic The present sequence

ô 1 CPDLVCYTDYLQTVICILEMMNIAPSTLTLTWQDQYEELXDEATSCSLHRSAHNATHATY 60 0; Gaps Length 538; 0; Indels 100.0%; Score 1195; DB 4; 100.0%; Pred. No. 1.6e-114; ive 0; Mismatches 0; Best Local Simitaricy Matches 218; Conservative Similarity Query Match Best Local &

à d

20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79

```
180
                      139
                                                                                                                                                                                                                                                                             antipsoriatic; antiinflammatory; immunosuppressive; cytostatic; virucide; antirheumatic; antiarthritic; antidiabetic; antithyroid; dermatological; nephrotropic; antibacterial; tuberculostatic; antileprotic; antipyretic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New interleukin-9/interleukin-2 receptor-like polypeptides and polymucleotides for diagnosing, treating respiratory, T-lymphocyte related disorders and disorders associated with lung, colon, kidney and
            TCHMDVEHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPFNVTVTFSGQYNISWR
                                                           140 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSSYELQ
TCHMDVFHFMADDIFSUNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                             SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                   Interleukin, IL-9; IL-2; 16445; antiasthmatic; antiallergic; human;
                                                                                          VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                               200 VRAGPMPGSSYQGTWSEWSDPVIPQTQSEBLKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 31-33; 54pp; English.
                                                                                                                                                                                                                                                                                                                 antiulcer; gene therapy; receptor.
                                                                                                                                                                        ABB81960 standard; protein; 538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-1999; 99US-00313913.
                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001; 2001US-00965313.
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-655832/70:
                                                                                                                                                                                                                                           Human 16445 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphoid tissues.
                                                                                                                                                                                                                                                                                                                                                              US2002090680-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABQ79536
                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                      25-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodge MR;
                      80
                                            121
                                                                                                                                                                                               ABB81960;
 61
                                                                                          181
                                                                                                                                                   RESULT 10
                                                                                                                                                                ABB81960
                셤
                                            ઠે
                                                                셤
                                                                                         ठ
                                                                                                              셤
```

```
AAE13726 standard; protein; 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                       Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB13726;
                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
   88888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                     ö
                                                                                                                                      120
                                                                                                                                                  80 TCHMDVFHFWADDIFSVNITDQSGNYSQEGGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                  140 SDYEDPAFYMLKGKLQYELQYENGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                  SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                           9
                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new murine \mathrm{MU}-1 protein, a meanatopoistin receptor auperfamily chain, comprising a fully defined sequence of 529 amino acids (\mathrm{AMU1})1915) as given in the specifications or fragment of protein having \mathrm{MU}-1 biological activity. The molecules of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide, useful for identifying compounds binding to MU-1, and for treating multiple sclerosis, rheumatoid arthritis, diabetes and asthma, comprises the isolated murine MU-1 protein, and a hematopoietin
                                                                                                                                                                                                                                                                                                                                                                             Human MU-1 haematopoietin receptor superfamily chain protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins M;
                                                                                                              20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                     61 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                        CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                   Human; MU-1; haematopoietin receptor superfamily chain; thyroiditis; immune deficiency; anaemia; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; pulmonary inflammation; insulin dependent diabetes mellitus; nutritional supplement; cytokine receptor family.
                                                                    ö
                                              ; DB 5; Length 538;
1.6e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowe
                                                                                                                                                                                                                               VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                    200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitters MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237. .254
/note= "Transmembrane domain"
                                          100.0%; Score 1195;
100.0%; Pred. No. 1.6
:ive 0, Mismatches
represents a human 16445 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 4; 59pp; English.
                                                                                                                                                                                                                                                                                                            AAU11912 standard; protein; 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2001; 2001WO-US015395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00569384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma, comprises the isola
receptor superfamily chain.
                                                                                                                                                                                                                                                                                                                                                         09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unger MJ,
                                                                  Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 2002-062239/08.
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS17248.
                        Sequence 538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200185792-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Donaldson DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001
                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                    AAU11912;
                                                                                                                                                                                                                               181
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                 AAU11912
 ខ្លង់ខ្ល
                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                            셤
                                                                                                                                     ઠે
                                                                                                                                                           d
                                                                                                                                                                                  ò
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                   원
```

```
invention may exhibit cytokine, cell proliferation or cell
differentiation activity and may also exhibit immune stimulating or
immune suppressing activity and can be useful in the treatment of various
immune deficiencies and disorders including severe combined
immune deficiencies and disorders including severe combined
immunodeficiency (SCID). Another use of the invention is treating
autoimmune disorders such as connective tissue disease, multiple
culcimmune disorders use eythematcosus, recumatoid archritis,
clerosis, systemic lupus erythematcosus, recumatoid archritis,
clabees mellitus, and autoimmune inflammatory eye disease. The invention
is useful for the treatment of myeloid or lymphoid cell deficiencies and
in treating various anaemias or for use in conjunction with
is useful for the treatment of myeloid or lymphoid cell deficiencies and
in treating various anaemias or for use in conjunction with
precursors and/or erythroid cells. The polynucleotides and proteins can
also be used as nutritional sources or supplements. The present protein
captuence represents the human MU-1 haemopoietin receptor superfamily
chain. MU-1 is also a member of the cytokine receptor family. This
sequence was used in the invention for the characterisation of previously
unknown members of the haematopoietin receptor superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic; inflammatory disorder; haemostatic; cell proliferation; immune disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; myasthemia gravis; systemic lupus erythematosus; ZiB; diabetes; aethma; ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 CPDLVCYTDYLGTVICILEMWNLHPSTLTLTMQDQYBELKORATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TCHMDVFHFMADDIPSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1195; DB 5;
100.0%; Pred. No. 1.6e-114;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192. .202
/note= "Penultimate Btrand region"
214. .218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human soluble Zalphall cytokine receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20. .538
|abel= Mature_Zalphall_protein
20. .237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Cytokine binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= Domain_linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $
```

Ą

(first entry)

```
AAU11978 standard; protein; 538
                                                            09-APR-2002
                                     AAU11978;
쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDYEDPAFYMLKGKLÓYELGYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELG 199
                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated soluble zalphall cytokine receptor polypeptide and their CDNA molecules. Zalpha proteins are useful for inhibiting or antagonising the ligand activity-induced proliferation of haematopoietic cells and haematopoietic cells progenitors preferably lymphoid cells which are natural killer cells or cytocoxic T cells. Salpha is useful for treating immune and inflammatory disorders, for reducing proliferation of neoplastic B or T cells, for suppressing an immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthitis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus (SLB) and diabetes; sepsis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble Zalphall cytokine receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                         Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 CPDLVCYTDYLQIVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                Nelson AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1195; DB 5; Length 538; Best Local Similarity 100.0%; Pred. No. 1.6e-114; Matches 218; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                               Holly RD,
                                               Intracellular_signalling_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRAGEMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237
                                                                                                                                                                                                                                                                                Presnell SR,
                                                                                               'note= "Box II signalling site"
                                                            267. .273
/note= "Box I signalling site"
   /label= Transmembrane_domain
256.538
/label= Intra-
                                                                                                         519. .522
/label= STAT3_binding_site
                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 172-173; 243pp; English
  'note= "WSXWS motif"
                                                                                                                                                                                                                                                                                West JW,
                                                                                                                                                                                                                    05-APR-2000; 2000US-0194731P.
28-JUL-2000; 2000US-0222121P.
                                                                                                                                                                                             03-APR-2001; 2001WO-US010872
                                                                                   101. 304
                                                                                                                                                                                                                                                         ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                Novak JE,
                                                                                                                                                                                                                                                                                                        WPI; 2002-025898/03.
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD22918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 538 AA;
                                                                                                                                               WO200177171-A2
                                                                                                                                                                                                                                                                                 Sprecher CA,
                                                                                                            Binding-site
                                                                                                                                                                       18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                Domain
                                      Domain
                                                             Region
                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
The present invention relates to the isolation of a novel cytokine, zalphall Ligand and the polymucleotide encoding it. The invention also gives the sequence for the zalphall receptor and the polymucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation of encoding it. The zalphall Ligand polypeptide stimulates proliferation of natural killer (NR) cells or NR cell progenitors, the activation of NR cells, proliferation of B-cells stimulated with anti-Ch40 antibodies, stimulates an antigenic response in a mammal, and reduces proliferation of B-cells stimulated with anti-IgM antibodies. The zalphall Ligand polymucleotides can bind to zalphall Ligand epitopes. The zalphall Ligand polymucleotides can can in gene therapy. Zalphall Ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence represents human zalphall receptor polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New zalphall ligand polypeptides and polymucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCHMDVFHFWADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 CPDLVCYTDYLQTVICILEMWNIHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                       Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; B-cell proliferation; anti-tumour response; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Řβ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 1195; DB 5; Length Ebest Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 218; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DC, Holly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA, Foster DC
7, Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 191-194; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sprecher CA
Nelson AJ,
Human zalphall receptor polypeptide
                                                                                                                                                                           immunostimulant; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0123547P.
99US-0123904P.
99US-0142013P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-2000; 2000US-00522217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presnell SR,
Johnston JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-040208/05
N-PSDB; AAS20642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigenic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                 US6307024-B1
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novak JE,
Gross JA,
```

ö

9 79 o

```
The invention relates to a novel method for treating or preventing an arthritic disorder in a subject. The method involves administering to the subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antergentiate optionally in combination with another therapeutic agent, to inhibit or reduce immune cell activity in the subject. The method is also useful for treating or preventing cancer or an infectious disorder, in a subject, by administering IL-21/IL-21R agonist, to increase immune cell activity. The method of the invention has antirheumatic, antiarthritic, osteopathic, antibociatic, cytostatic, antibacterial, virtucide, antipacatabile, antibociatic, antisathmatic, antiallergic, antianaemic, hepatotropic, antiuloer, antiallergic, antianaemic, hepatotropic, antibulity and antihinflammatory activity. The method is useful for treating or preventing an arthritic disorder such as rheumatoid arthritis, osteoarthritis, psoriatic arthritis, juvenile rheumatoid arthritis, and also cancer such as solid arthritis, antiple or antiple or antiple or metastatic lesion, or an infectious and answer and also cancer such as solid antiple of sorder such a bacterial, viral or parasitic infection in a mammal, the method of the invention containing an antigen to elicit a protective immune response in a subject against the antigens.

The antigen is from a pathogen such as virus, bacterium or protozoan, or
                                                                                                                                                                                                                                                                                                                                                                arthritic disorder, interleukin-21, IL-21, IL-21 receptor, IL-21R, immune cell activity; cancer, infectious disorder, antiheumatic, antiantic; osteopathic; antipsoriatic; cytostatic; antibacterial; virucide, antiparasitic; immunosuppressive, antidiabetic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating or preventing arthritic disorder, cancer or infectious disorders in a subject, involves administering a modulator of interleukin-21 or its receptor which modulate immune cell activity.
SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRLISVDSRSVSLIPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; antiulcer; antiallergic; antianaemic; hepatotropic; antithyroid; antinflammatory; immune response; immune disorder; autoimmune disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DA, Larsen G;
Witek JS, Kasaian MT;
                                                              VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                              200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΣX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins P
Dunussi P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 40; Fig 2B; 176pp; English.
                                                                                                                                                                                                     ABR61402 standard; protein; 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2001; 2001US-00972218.
17-APR-2002; 2002US-0373746P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2002; 2002WO-US029839
                                                                                                                                                                                                                                                                                     12-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                           NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitters MJ,
ND, Lowe LD,
                                                                                                                                                                                                                                                                                                                         IL-21R SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carter L, Whitters
Donaldson DD, Lowe
Ungar M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-430146/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACC80861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003028630-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2003.
                                                              181
                                                                                                                                                                                                                                              ABR61402;
                       140
                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                              RESULT 14
                                                                                                                                                                                    ABR61402
                                                            ò
```

```
New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and diabetes.
from cancer or tumour cell antigen, or expressed on the surface of cancer cell. An alternative method of the invention is useful for modulating the activity of immune or haematopoietic cells and thus to treat or prevent a variety of immune disorders, such as autoimmune diseases, for example diabetes mellitus, multiple sclerois, myasthenia gravis, systemic lupus erythematous, dematitis, ulcer, asthma. allergic asthma, anaemia, hepatitis, Graves's disease, graft versus host disease, and scleroderma. The present sequence is used in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                     80 TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 139
                                                                                                                                                                                                                                                                                                                                                                                                                           SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRKTISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISYDSRSVSLLPLEFRKDSSYELQ 199
                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; diabetes; human; zalphall receptor; IL-21 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides and polypeptides of interleuki 21 (IL-21) antagonists, that bind with specificity and exhibit an BCS0 that is not detectable in receptor binding studies. The antagonists of
                                                                                                                                                                                                                                                                                                            20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTTWQDQYEELKDEATSCSLHRSAHNATHATY
                                                                                                                                                                                                                                                                                                                                                    TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR
                                                                                                                                                                                                                                                                           1 CPDLVCYTDYLQTVICILEMWNLHPSTLTTTWQDQYBBLKDEATSGSLHRSAHNATHATY
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                    538;
                                                                                                                                                                                                    DB 6; Length
                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEBLKEGWNPH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRAGPMPGSSYQGTWSEWSDPVIPQTQSEELKEGWNPH 218
                                                                                                                                                                                                  100.0%; Score 1195; DB 6; 100.0%; Pred. No. 1.6e-114;
                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human interleukin-21 (IL-21) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 65-67; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE14939 standard; protein; 538 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novak JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-2002, 2002WO-US034502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001, 2001US-0337586P
                                                                                                                                                                                                                                            Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                West JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-441547/41.
                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD47859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003040313-A2.
                                                                                                                                                                   Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE14939;
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAE14939
 8888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

the invention have mutations in the D helix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide, such as cancer, inflammatory and autoimmum disorders, including rheumatorid arthritis, multiple soletosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 receptor (originally designated zalphall receptor) 8888888888888888

Sequence 538 AA;

Gaps ; 0 Length 538; Query Match
100.0%; Score 1195; DB 7; Length 5
Best Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 218; Conservative 0; Mismatches 0; Indels ઠે

20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79 1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY

g

g

g ò g

200 VRAGPMPGSSYQGTWSBWSDPVIFQTQSBELKEGWNPH 237

3, 2004, 12:35:38 Search completed: March Job time: 53.0065 secs

```
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-052-205-7
                                                                           March 3, 2004, 12:33:10 ; Search time 16.3007 Seconds (without alignments) 734.770 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                      1 LNTTILTPNGNEDTTADFFL.....QHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                  Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                             Minimum DB seg length: 0 Maximum DB seg length: 2000000000
                                                                                                                               US-09-825-561A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199.5
199.5
199.5
1799.5
178
                                                                                                                                                          Sequence:
                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
```

Sequence 32, Appl Sequence 4, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 97, Appli Sequence 97, Appli Sequence 2, Appli Sequence 115, Appl Sequence 3, Appli Sequenc
US-09-313-942-32 US-09-851-986-4 US-09-851-985-2 US-07-960-389-2 US-08-243-010-6 US-08-351-149-6 US-08-351-149-6 US-08-351-149-6 US-08-351-149-6 US-09-522-217-97 US-09-522-217-97 US-10-295-723-97 US-10-295-723-97 US-09-522-217-115 US-09-522-217-115 US-09-522-217-115 US-09-523-246-115 US-09-233-246-115 US-09-233-246-115 US-09-233-246-115 US-09-233-246-115 US-09-233-246-115
ਚਾ ਚਾ ਚਾ ਜ ਜ ਜ ਜ ਜ ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ਚਾ ਜ
C 20 0 8 10 4 4 4 0 0 0 0 0 10 10 10 10 10 10 10 10 10 10
8 4 4 4 4 8 8 8 8 6 6 6 6 6 6 6 6 6 6 6
8444 11 14 444 12 14 14 14 14 14 14 14 14 14 14 14 14 14
30000000000000000000000000000000000000

ALIGNMENTS

```
US-08-05-20-07

Sequence 7 Application US/0805205

Patent No. 5510259

GENERAL INFORMATION:

PAPLICANT: TAKESHITA, TOSHITACA

APPLICANT: TAKESHITA, TOSHITACA

APPLICANT: SHAWMEA, TASHITACA

APPLICANT: SHAWMEA, TOSHITACA

APPLICANT: HAMTRA, TOSHITACA

CONTRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIRE & NEUGTADT, ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, SUITE 400

CITT: ALINGTON

CITT: ALINGTON

STARE: VITSHITACA

COMPUTER: IBM PC COMPATIBLE FORM:

MEDIUM TYPE: PLOSTY disk

MEDIUM TYPE: PLOSTY disk

MEDIUM TYPE: PLOSTY MISK

MEDIUM TYPE: 19920425

CUMPARAT FARDABLE FORM:

MEDIUM TYPE: 19920425

CUMPARAT SHAMMEN: US-05/MS-05

CUMPARAT SHAMMEN: US-05/MS-05

CUMPARAT APPLICATION NUMBER: US-0615-0X

TELEBONE: (709) 413-402-0

TELEBONE: (709) 413
```

```
US-08-052-205-4
                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                     셤
                                                                                                                                    셤
                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                              TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                     121 TOMIKLONIVIPWAPENITLHKISESQLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                       61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                       121 TOMLKLONLVIPWAPENLTLHKLSESQLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                              9
                                                                                                                                         1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                   1 INTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEBVQCFVFNVEYMVCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                        DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: TASAO, HIRONOBU
APPLICANT: SASO, HIRONOBU
APPLICANT: SHIMAMURA, MASHARA
APPLICANT: SHIMAMURA, POSHIRO
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNI
APPLICANT: HAMURO, HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
     Length 347;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: P.C. STRET: 1755 S. Jefferson Davis Highway, Suite 400 STRET: 1755 S. Jefferson Davis Highway, Suite 400 STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPENATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATE: US/08/595,974
FILING DATE: US/08/EB-1996
  Score 1288; DB 1;
Pred. No. 1.4e-118;
Query Match
100.0%; Score 1288; 1
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 232; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-ARR-1993
APPLICATION NUMBER: UP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NOW-575608man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08595974
Patent No. 5705608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1(TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-FEB-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-595-974-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-595-974-7
                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
ö
                                                                                                                                                                                                                                                         61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCOLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                             121 TOMIKLONIVIPWAPENLTILHKISESQLEINWNNRFILNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                       1 INTTILTPNGNEDITADPPLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 60
                                                                                                                                                                                                                                                                                                                                        121 TQMLKLQNLVIPWAPENLTLHKLSESQLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                              61 INLILHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKBIHLYQTFVVQLQDPREPRRQA
                                                                                                         1 INTTILIPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SUZUKI, MASATAKA
APPLICANT: SUZUKI, MANBU
APPLICANT: SUGUKICS: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: D.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                              DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                        ó
Score 1288; DB 1; Length 347; Pred. No. 1.4e-118; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk

COMDUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/052,205

FILING DATE: 19930422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1288; DB 1;
Pred. No. 1.5e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
        Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 413-2220
TELEX: 246855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 369 amino acids
AMINO ACID
                                                           Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
```

```
232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
US-09-191-786-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
  Matches
                                      ò
                                                                         ď
                                                                                                                 ò
                                                                                                                                                        ద
                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                      INLTLHYWYKNSDNDKVOKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                     TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                        TOMLKLONLVIPWAPENLTLHKLSESQLELNWANRFLAHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                        TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQXKEIHLYQTFVVQLQDPREPRRQA 142
                                                                      LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                      1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SUCHIA, MANABO
APPLICANT: SUCHIA, MANABO
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
TOWNERR OF SEQUENCES: 21
CORRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPATIBLE
COMPUTER: EN PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                     DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 369;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PALLCATION NUMBER: US/08/595,974
PILING DATE: 06-PEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1288; DB 1;
Pred. No. 1.5e-118;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: UP 104947/1992
FILING DATE: 23-APR-1993
ATTORNEY/AGENT TREORMATION:
NAME: Oblon, No. 5705608man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Oblon, No. 5705608man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAKESHITA, TOSHIKAZU
ASAO, HIRONOBU
NAKAMURA, MASATAKA
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08595974
Patent No. 5705608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHIMAMURA, TOSHIRO
SUZUKI, MANABU
HAMURO, JUNJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1
TELEMONINICATION INFORMATION
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGAMURA, KAZUO
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248855 OPAT UINFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-595-974-4
                                                                                                                                                                                                                                            143
                                                                                                                    19
                                                                                                                                                            83
                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                       203
Matches
                                      ò
                                                                             셤
                                                                                                                      ò
```

```
143 TOMIKLONLVIPWAPENLTLHKLSESOLELNWNNRFLNHCLEHLVOYRTDWDHSWTEOSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TNLTLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                               83 TNLTLHYWYKNSDNDKVOKCSHYLPSEEITSGCOLOKKEIHLYQTFVVOLODPREPRRQA
                                                                                                                                                                                                                                                  121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEQSV
                                               1 INTILLTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVBYMNCTWNSSSEPQP
                                                                                                                                               61 INLTLHYWYNNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                               23 INTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFVVBYMNCTWNSSSEPQP
  Gaps
                                                                                                                                                                                                                                                                                                                                                  181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
ő
                                                                                                                                                                                                                                                                                                                                                                                       DYRHKESLPSVDGQKRYTFRVRSRFNPLCGSAQHWSBWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09191786
Patent No. 6372898
GENERAL INFORMATION:
APPLICANT: Cacalano, Nicholas A.
APPLICANT: Johnston, James A.
TITLE OF INVENTION: Mammalian Protein Variants and Methods
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTTER: IBM PC Compatible
COMPOTTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,786
FILING DATE: 11.NOV-1998
CLASSIFICATION: 435
ATTORNEY/AGBWT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REPERENCE/DOCKET NUMBER: DX0920
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304-1104
COMPUTER REDABLE PORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 496-120
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
```

```
RESULT 9
US-09-189-129-2
                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TNLTLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                          TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                      143 TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 INLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 82
                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09313942

Sequence 20, Application US/09313942

Patent No. 6472179

GENERAL INFORMATION:
PAPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: AND USING

TITLE OF INVENTION: AND USING

TITLE OF THE REPERENCE: 1999-05-19

CURRENT APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-29

PRIOR FILING DATE: 1999-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09313942

Patent No. 647219

GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
TITLE OF INVENTION: AND USING
TITLE OF INVENTION: AND USING
TITLE OF TAPPLICATION NUMBER: US/09/313,942
CURRENT APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR PILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                  DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1288; DB 4; 100.0%; Pred. No. 3.6e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-313-942-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OKGANISM: HOT
US-09-313-942-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 20
                                                                                                                                  181
                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
83
                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                          ઠે
                                                                                    g
                                                                                                                                  ò
                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੇ
```

```
61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TOMIKLONIVIPWAPENLILHKISESQLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TOMIKLONLVIPWAPENLTIHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNRFLNHCLEHLVQYRTDWDHSWTEGSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 INLTLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKBIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 INTTILIPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSPQP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT'R REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
FRICA PAPLICATION NUMBER: 09/313,942
FRICA FILING DATE: 1999-05-19
FRICA RILING DATE: 1999-05-15
FRICA REPLICATION NUMBER: 09/313,942
FRICA RILING DATE: 1999-05-15
FRICA REPLICATION NUMBER: 09/313,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LNTTILIPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 INTILLTPNGNEDITADFFLTTMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DYRHKFSLPSYDGOKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 DYRHKFSLPSVDGQKRYTFRVRSRPNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                           Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1288; DB 4; Length 694; Best Local Similarity 100.0%; Pred. No. 3.6e-118; Matches 232; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1288; DB 4;
100.0%; Pred. No. 3.6e-118;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 22, Application US/09313942; Patent No. 6472179
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 232; Conservative
; SEQ ID NO 18
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-313-942-22
```

```
61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOMIKLONIVIPWAPENLTLHKLSESOLELNWANRFLAHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 TOMLKIONLVIPWAPENLTLHKISESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYRHKFSLPSVDGQKRYMFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.5%; Score 1282; DB 4; Length 482; 99.6%; Pred. No. 8.4e-118; tive 0; Mismatches 1; Indels
                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Benjamin, Christopher D
APPLICANT: Hession, Catherine A
APPLICANT: Howitty, Adrian
TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge Center
CITY: Cambridge Center
STATE: MASSachusetts
COUNTRY: USA
ZITE: 14 Cambridge Center
STATE: Diogen, Inc.
STREET: 14 Cambridge Center
CONPUTER: IBM PC Compatible
CONPUTER: DatentIn Release #1.0, Version #1.30
CONPUTER: PatentIn Release #1.0, Version #1.30
CONPUTER: OS-MAY-1997
APPLICATION NUMBER: A006 PCT CIP
FILING DATE: OS-MAY-1997
APPLICATION NUMBER: A006 PCT CIP
FILING DATE: OS-MAY-1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 34,199
REFERENCE/DOCKET NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A0169
TELEFAX: 617 679-2838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: A 182 amino acids
LENGTH: A 182 amino acids
Sequence 2, Application US/09189129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 482 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ANTI-SENSE: NO
US-09-189-129-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
```

RESULT 10 US-08-052-052-11 ; Sequence 11, Application US/08052205 ; Patent No. 5510259

GENERAL INFORMATION

```
61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 INLILHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 INTTILTPNGNEDÍTADFFLÍTAPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVOCFVFNVEYMVCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAWURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                            NUMBER OF ESCUENCES:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: P.C.
STREET: P.C.
STREET: Virginia
COUNTRY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
CMPUTER: PRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
FILING DATE: 19930422
CLASSIFICATION NUMBER: US/08/052,205
FILING DATE: 1993042
CLASSIFICATION NUMBER: 27 10 104947/1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 511025man F.
RESTERANCE/DOCKET NUMBER: 24,618
REPERENCE/DOCKET NUMBER: 24,618
REPERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
MART OBLON, NO. 511025man F.
REPERENCE/DOCKET NUMBER: 24,618
REPERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%; Score 1277; DB 1; Length 2 100.0%; Pred. No. 9.2e-118; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-595-974-11
Sequence 11, Application US/08595974
Patent No. 5705608
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 413-300
TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.1
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-052-205-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ਨੇ
```

APPLICANT: SHINAMURA, APPLICANT: SUZUKI, MANABU
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMIRO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.

CITY: Arlington STATE: Virginia COUNTRY: U.S.A.

us-09-825-561a-4.rai

```
APPLICANT: NALAWANTA, TOSHIKO,
APPLICANT: SHIMAMURA, TOSHIKO
APPLICANT: STAUKI, MANABU
APPLICANT: STAUKI, MANABU
APPLICANT: HAWTRO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
CORRESPONDENCE ADDRESS:
ADDRESSEE: 08LON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                           ASAO, HIRONOBI
                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                      inear
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-595-974-11
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
CORRANT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: UP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 10-615-0X
TELECOMMULCATION INFORMATION:

413-2220

TELEFAX:

TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS

, MOLECULE TYPE: protein US-08-052-205-9

linear

TOPOLOGY:

```
143 TOMLKLONLVIPWAPENLITLHKLSBSQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                       61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRQA 120
                                                                                                                                                                                                                                                                      83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDFREPRRQA 142
                                                                                                                                                                                                                                                                                                                                  121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFILNHCLEHLVOYRTDWDHSWTEQSV 180
                                                                                                                                             23 LNTTILIPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 82
                                                                                                                1 LNTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                           Gaps
                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 252
Query Match 99.1%; Score 1277; DB 1; Length 252; Best Local Similarity 100.0%; Pred. No. 1e-117; Matches 230; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08595974; Patent No. 5705608; GAMERAL INFORMATION: APPLICANT: SUGAMURA, KAZUO APPLICANT: TAKESHITA, TOSHIKAZU APPLICANT: ASAO, HIRONOBU APPLICANT: NAKAMURA, MASATAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-595-974-9
                                                                                                                ò
                                                                                                                                                                  Я
                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                            윰
                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                       ઠ
```

121 TOMEKLONLVIPWAPENLTLHKLSESQLELNWNNRFINHCLEHLVOYRTDWDHSWTEQSV 180

121

В ò 181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230

Sequence 9, Application US/08052205 Patent No. 5510259 GENERAL INFORMATION: APPLICANT: SUGAMURA, KAZUO APPLICANT: TAXESHITA, TOSHIKAZIT

US-08-052-205-9

181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230

1 LNTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 1 LNTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSPQP

Gaps

.; 0

Length 230; 0; Indels

99.1%; Score 1277; DB 1; L 100.0%; Pred. No. 9.2e-118; ive 0; Mismatches 0;

Query Match Best Local Similarity 100.0 Matches 230; Conservative

ò 쉽 ò B ઠે

```
61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOMIKLONLVIPWAPENLTLHKISESQLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 TQMLKLQNLVIPWAPBNLTLHKLSBSQLBLNWNNRFLNHCLBHLVQYRTDWDHSWTBQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 TNLTLHYWYKNSDNDKVQKCSHYLFSEBITSGCQLQKKBIHLYQTFVVQLQDPRBPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LNTTILIPNGNEDITADFFLITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
APPLICANT: SHIWAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO,
JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.1%; Score 1277; DB 1; Length 252; Best Local Similarity 100.0%; Pred. No. 1e-117; Matches 230; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION WHERE: US/08/595,974
FILING DATE: 20-APR-1993
APPLICATION NUMBER: US 08/052,205
FILING DATE: 21-APR-1993
APPLICATION NUMBER: US 08/052,205
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                         STREET: 1755 S. Jefferson Davis Hi
CITY: Arlington
STATE: Virginia
COUNTY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPACTIONS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 252 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248855 OPT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-595-974-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

PILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGBWT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 26,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1212-751-6849

TELERAX: 212-751-6849 TELEX: 421792 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

DESCRIPTION: PROTEIN

MOLECULE TYPE:

TOPOLOGY:

AMINO ACID
Y: UNKNOWN

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,224

COUNTRY: USA ZIP: 10154 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK

SSEE: MORGAN & FI T: 345 PARK AVE. NEW YORK : NEW YORK

CORRESPONDENCE ADDRESS:

```
62 NLTLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKEIHLYQTFVVQLQDFREPRRQAT 121
                                                                                                                                                                                                                                                                                                                                           84 NITLHYRYKVSDNNTFQECSHYLFSKEITSGCQIQKEDIQLYQTFVVQLQDFQKPQRRAV 143
                                                                                                                                                                                                                                                                                                                                                                                                                122 OMLKLONLVIPWAPENLTIHKLSESQLEINWINRFL-NHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 69, APPLICATION:
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTINES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF EXPENTION: ASCID
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                 2 NITILIPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPT
                                                                                                                                                                                                                                              24 SSKVLMSSANEDIKADLILISTAPEHLSAPTLPLPEVQCFVFNIEYMNCTWNSSBEPQAT
                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 369;
                                                                                                                                                                 Indels
                                                                                                               Query Match 66.3%; Score 853.5; DB 2; Best Local Similarity 67.2%; Pred. No. 8e-76; Matches 156; Conservative 33; Mismatches 42;
OMGANISM: MURINE
;
US-08-424-224-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
PCT-US94-02891-69
                                                                                                                                                                                                                                                                                                                                                                   임
                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
```

CDNA AND

WARREN J. MURINE IL-2R USES THEREOF

GENERAL INFORMATION:
APPLICANT: LEGNARD, W
TITLE OF INVENTION: OTHER OF SEQUENCES:

US-08-424-224-2 ; Sequence 2, Application US/08424224 ; Patent No. 5912173

CORRESPONDENCE ADDRESS:

```
144 QKLNLQNLVIPRAPENLTLSNLSBSQLELRWKSRHIKERCLQYLVQYRSNRDRSWTELIV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 NLTLHYRYKVSDNNTFQBCSHYLFSKEITSGCQIQKEDIQLYQTFVVQLQDPQKPQRRAV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 OMLKLONLVIPWAPENLTLHKLSESOLELNWANNRFL-NHCLEHLVOYRTDWDHSWTEOSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NITILIPPNGNEDITADFFLITMPIDSLSVSTLPLPEVOCFVFNVEYMNCTWNSSSEPQPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 SSKVLMSSANEDIKADLILTSTAPEHLSAPTLPLPEVQCFVFNIEYMNCTWNSSSEPQAT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 DYRHKFSLPSVDGOKRYTPRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
66.3%; Score 853.5; DB 5; Length 369;
Best Local Similarity 67.2%; Pred. No. 8e-76;
Matches 156; Conservative 33; Mismatches 42; Indels 1
CURTABLE NORGAN & FINNEGAN
STREET: 345 PARK AVE.
CUITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: ELDOPY DISK
COMPUTER: ELDOPY DISK
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/031,435
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 26,728
FILING DATE: 14-SEPT-1993
APPLICATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELEPAN: 212-758-4800
TELEFAN: 212-751-6849
TELEPAN: 212-751-6849
TYPE: AMINO ACID
TOPOLOGY: NURNOWN
MOLECULE TYPE:
DESCRIPTION: PROTEIN
TYPE: AMINO ACID
TOPOLOGY: NURNOWN
MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
INTOWNING MURINE
INITURING MURINE
INITURING MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: March 3, 2004, 12:39:55 Job time: 17:3007 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US94-02891-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

sus scrofa gallus gall homo sapien

Q90375 Q9jbx3 Q9jbx3 Q9jbx3 Q02092 Q02092 Q08351 Q08351 Q92859 P52835

mus musculu homo sapien oreochromis homo sapien flaveria bi

columba liv mus musculu rattus norv musculu

```
TISSUES—S-Cell;
MEDLINE-21388257; PubMed=12477932;
K TISSUES—Cell;
MEDLINE-21388257; PubMed=12477932;
K Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Alschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
Alschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
Alschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Baha S.S., Inquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villahon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Halvejley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                         D31785;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
115-MAR-2004 (Rel. 43, Last amnotation update)
Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-Cytokine receptor common (IL-2R gamma chain) (P64) (CD132 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANTS XSCID ASP-114 AND ASN-153.
MEDLINE-94004847; PubMed-8401490;
Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
Willard H., Henthorn P.S.;
"The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
in X-linked severe combined immunodeficiency, SCIDXI.";
Hum. Mol. Genet. 2:1099-1104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;
MEDLINE=91293887; PubMed=8514792;
Noguchi M., Adelstein S., Cao X., Leonard W.J.;
"Characterization of the human interleukin-2 receptor gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,
Munakata H., Nakamura M., Sugamura K.;
"Cloning of the gamma chain of the human IL-2 receptor.";
Science 257:379-382(1992).
                                                                                                                                                                                                                                                                                               PRT; 369 AA
                                                                                                                                                                                                                      ALIGNMENTS
             GHR COLLI
121R MOUSE
116B RAT
116A PIG
GHR CHICK
GHR THOMAN
TPOR MOUSE
PRLR HUMAN
                                                                                                                                       PRLR OREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 268:13601-13608(1993).
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 CYRG HUMAN
CYRG HUMAN
 homo sapien
mus musculu
homo sapien
homo sapien
homo sapien
gallus gall
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu bos taurus homo sapien mus musculu mus musculu mus musculu mus musculu rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
cervus elap
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mus musculu
oncorhynchu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meleagris g
columba liv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bos taurus
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rattus norv
                                                                                                       March 3, 2004, 12:25:04; Search time 8.71896 Seconds (without alignments) 1385.519 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                     1 INTTILTPNGNEDTTADFFL......QHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95118
Q14627
Q14627
Q09630
P32927
P32927
P15509
Q91094
P16382
P16382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q28172
Q9hbe5
P21183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O8cii9
P26954
O8r488
P22272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              028235
001344
P40189
P14784
008501
P22273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  931785
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
MOUSE
MOUSE
CEREL
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAT
RAT
SHEEP
                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
HUMAN
CHICK
HUMAN
MELGA
COLLI
MOUSE
MOUSE
BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCYRG | CCYRG 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILSR
CRL2
                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                       US-09-825-561A-4
1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt 42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110.5
109.5
109
108.5
                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                  Searched:
                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
```

```
Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X., Leonard W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94375038; PubMed-8088810;
Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
de Saint Basile G.;
"Detection of three nonsense mutations and one missense mutation in
the interleukin-2 receptor gamma chain gene in SCIDX1 that
differently affect the mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-STRUCTURE MODELING OF 57-248.
MEDLINE=95111955; PubMed=7529123;
Bamborough P., Hedgecock C.J., Richards W.G.;
"The interleukin-2 and interleukin-4 receptors studied by molecular modelling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A., de Saint Basile G.; "Defective human interleukin 2 receptor gamma chain in an atypical chromosome-linked severe combined immunodeficiency with peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishli N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya Konno T., Maeda M., Uchiyama T., Sugamura K.; Ishling M., Uchiyama T., Sugamura K.; Ishling of mutant IL-2 receptor gamma-chains in patients with X-linked severe combined immunodeficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Interleukin-2 receptor gamma chain: a functional component of the
                                                                                             [5]
IDENTIFICATION AS A IL-4R SUBUNIT.
MEDLINE=94090315; PubMed=8266076;
KONGO, Takeshita T., Ishii N., Nakamura M., Watanabe S.,
Arai K.-I., Sugamura K.;
Arai K.-I., Sugamura K.;
"Sharing of the interleukin-2 (IL-2) receptor gamma chain between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Interleukin-Z (IL-Z) receptor gamma chain mutations in X-linked severe combined immunodeficiency disease result in the loss of high-affinity IL-Z receptor binding.";

Eur. J. Immunol. 24:475-479(1994).
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                 MEDLINE=94090317; PubMed=8266078; Ruseall S.M., Kkegan A.D., Harada N., Nakamura Y., Noguchi M., Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E., Leonard W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
MEDLINE=94130970; Pubmed=829698;
Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
de Saint Basile G.;
                                                                                                                                                                                                                                                                                                                                                                             "Interleukin-2 receptor gamma chain: a functional
                                                                                                                                                                                                                                                                              IDENTIFICATION AS A IL-4R SUBUNIT. MEDLINE=94090317; PubMed=8266078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION AS A IL-7R SUBUNIT. MEDLINE=94090316; PubMed=8266077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94300093; PubMed=8027558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT XSCID ASN-39.
MEDLINE=95023932; PubMed=7937790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunol. 153:1310-1317(1994)
                                                                                                                                                                                                                   receptors for IL-2 and IL-4.";
Science 262:1874-1877(1993).
                                                                                                                                                                                                                                                                                                                                                                                                interleukin-4 receptor.";
Science 262:1880-1883(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin-7 receptor.";
Science 262:1877-1880(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure 2:839-851(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differently affect the mR
Genomics 21:291-293(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT XSCID HIS-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT XSCID LYS-68
      RITER REPRESENTE EN REPRETE EN LE REPRESENTE EN LE REPRESENTE EN REPRESENTE EN LE REPRESENTE EN REPRESENTE EN R
```

the

component of

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBSINIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and probably also the IL13 receptors:
-1- SUBCELLIAR LOCATION: Type! I membrane protein.
-1- DISPASE: Defects in IL28Gare the cause of X-linked severe combined immunodeficiency (XSCID) (MIM:300400); also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agammaglobulinemia, Swiss.type i cytokine family of receptors.
SMILARITY: Belongs to the type i cytokine family of receptors.
Subfamily S.
SIMILARITY: Contains 1 fibronectin type III domain:
DATABASE: NAME-PROW; NOTB-CD guide, CD132 entry;
WWW-HRTP://ww.ncbi.nlm.nih.gov/prow/cd/cd132.htm".
DATABASE: NAME-ILZRGABSE, NOTE-K-linked SCID/mutation database;
WWW-hrtp://www.nbgri.nih.gov/DIR/GMBB/SCID/".
                                                                                                                                                                                                                                                                                                                                                                                              Puck U.M., Pepper A.E., Bedard P.-M., Laframboise R.; Puck U.M., Pepper A.E., Bedard P.-M., Laframboise R.; "Female germ line mosaicism as the origin of a unique IL-2 receptor agamma-chaim mutation causing X-linked severe combined immunodeficiency.", J. Clin. Invest. 95:895-899(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT XSCID GLN-285.
MEDLINE-97295088; PubMed=9150740; Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L., Cant A., Kinnon C., Incompany associated with a "B-cell-negarive severe combined immunodeficiency associated with a common gamma chain mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95190013; PubMed=7883865; Schmaltelieg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E., Dennay R.M., Dav. Leonard W.J., Noguchi M., Berg M., Rudloff H.E., Missense mutation in exon 7 of the common gamma chain gene causes moderate form of X-linked combined immunodeficiency."; J. Clin. Invest. 95:1169-1173 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT XSCID CYS-222.
WARIANT SP064061; PubMed=9399950;
Sharfe N., Shahar M., Roifman C.M.;
"An interleukin-2 receptor gamma chain mutation with normal thymus
[13]
VARIANTS XSCID CYS-226 AND HIS-226.
MEDLINE=95397841; PubMed=7668284;
PEDDER A.E., Buckley R.H., Small T.N., Puck J.M.;
Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
Two mutational hotspots in the interleukin-2 receptor gamma cha "Two mutational hotspots in the interleukin-2 receptor gamma cha gene causing human X-linked severe combined immunodeficiency.";
Am. J. Hum. Genet. 57:564-571(1995).
                                                                                                                                                              VARIANT XSCID SER-183.
WEDLINB=96013903; PubMed=7557965;
Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
Levinsky R.L., Kinnon C.;
"Screening for mutations causing X-linked severe combined
immunodeficiency in the IL-2R gamma chain gene by single-strand
conformation polymorphism analysis.";
Hum. Genet. 96:427-432(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Clin. Invest. 100:3036-3043(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97042245; PubMed=8900089;
Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Saint Basile G., Arbypical X.linked severe combined immunodeficiency due to apontaneous reversion of the genetic defect in T cells."; New Engl. J. Med. 335:1563-1567(1996).
                                                                                                                                                                                                                                                                                                                                                        VARIANT XSCID GLN-HIS-TRP-237 INS
MEDLINE=95164726; PubMed=7860773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet. 99:677-680(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT XSCID ARG-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . interleukins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 morphology.";
```

. .

×H

Natl. Acad. Sci. U.S.A. 91:9466-9470(1994)

cella." Proc. N

HEMATOPO REC S F1; 1

쉱

ਨੇ

8 8 8 8

ਨੇ

```
CYRG BOVIN
Q95118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma gene.
                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                DISULPID
                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                            DOMAIN
                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYRG_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            0
                                                                                                                                                                                                                 83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                  202
                                                                                                       9
                                                                                                                                              82
                                                                                                                                                                                                                                                                                                   143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                           23 LNTTILIPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                    61 INLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                          TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and probably also the IL13 receptors.
-1- SUBCELLIULAR LOCATION: Type I membrane protein.
-1- DISEASE: Defects in IL2RG are the cause of a canine X-linked severe combined immunodeficiency.
                                                                                                   1 INTILLIPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVBYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
MEDLINE=95130114; PubMed=7829104;
Henthorn P.S., Somberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
Felsburg P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cante iamiliaris (Jog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "IL-2R gamma gene microdeletion demonstrates that canine X-linked severe combined immunodeficiency is a homologue of the human
                                                                                                                                                                                                                                                                                                                                                           181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                             DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Common subunit for the receptors for a variety of interleukins.
                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequencian update)
Cytokine receptor common gamma chain precursor (Gamma-C)
[Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
                  Length 369;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Subfamily 5.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
               ; Score 1288; DB 1;
; Pred. No. 3.9e-99;
0; Mismatches 0;
               100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U04361; AAC48403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 23:69-74(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A55718; A55718.
             Query Match
Best Local Similarity
Matches 232; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYRG CANFA
P40321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease."
                                                                                                                                                                                                                                                                          121
```

InterPro; IPR002996; CRIA. InterPro; IPR008957; FN III-like. InterPro; IPR0083961; FN III. InterPro; IPR0033511; Hemtopoptn_S_F1. SMART; SM00060; FN3; 1.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                83 INLILHYWYKNSNDDKVQECGHYLPSREVTAGCWLQKEEIHLYETFVVQLRDPREPRRQS 142
                                                                                                                                                                                                                                                                                                                                                                                                                           TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TOMLKLONLVIPWAPENLTLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEOSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202
                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                 1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 a probably also the IL13 receptors.
-!- SUBCRILULAR LOCATION: The I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                 POTENTIAL.
CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYRHKRSLPSVDGQKRYTPRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96268473; PubMed=8672241;
Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
"Cloning and chromosomal mapping of bovine interleukin-2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Cytckine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Cell Biol, 15:453-459(1996),
-1- FUNCTION: Common subunit for the receptors for a variety
interleukins.
                                                                                                                                                                                                                                                                                            85.2%; Score 1097; DB 1; Length 373; 82.8%; Pred. No. 2.3e-83; ive 24; Mismatches 16; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subfamily 5.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                               03A0DE1F8B089D8B CRC64;
                                                  EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                          CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III. POTENTIAL.
                                                                                                                                                (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
                                                                                                                                                                                                            (GLCNAC. . .)
Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                             42516 MW;
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                    taurus (Bovine)
                                                                                                                                                                                                                                                                                                          Local Similarity
nes 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
```

Biochem. Biophys. Res. Commun. 193:356-363(1993)

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 SSEPQPNNLTLHYGYRNFNGADDKIQECGHYLFSEGITSGCWFGKKEIRLYETFVVQLQDP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 REPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 REHRKQPKQMLKLQDLVIPWAPENLTLRNLSEFQLELSWSNRYLDHCLEHLVQYRSDRDR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWITEQSVDYRHKFSLPSVDGQKRYIFRVRSRFNPLCGSAQHWSEWSHPIHWGSNISKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, InterP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LNPKFLTPSGNEDIGGKPGTGGDFFLTSTPAGTLDVSTLPLPKVQCFVFNVEYMNCTWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTILITINGNED-----TTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEPQPTNLTLHYWYKN-SDNDKVQKCSHYLFSBEITSGCQLQKKEIHLYQTFVVQLQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93277575; PubMed-8503926; Kunde M., Nakamura M., Sugamura K.; Kundo M., Takeshita T., Asao H., Nakamura M.; Sugamura K.; Cloning of the mouse interleukin 2 receptor gamma chain: demonstration of functional differences between the mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (F64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33CFAD9C9B032178 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%; Score 990.5; DB 1; 76.2%; Pred. No. 1.4e-74; cive 21; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                   Incerpro; IPR002996; CRIA.
Interpro; IPR008957; FN III-like.
Interpro; IPR003961; FN III.
Interpro; IPR003531; Hemtopoptn_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43037 MW;
                                                                                                                                                                                       EMBL; U33748; AAB07812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2004 (Rel. 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors.";
                                                                                                                                                                                                                    HSSP; P31785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYRG MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYRG_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL2RG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-FVB/N; TISSUE-salivary gland;

A trausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A trausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.P., Bhat N.K.,

Altschul S.F., Zeeberg B.J., Buetow K.H., Schaefer C.P., Bhat N.K.,

A distrement D., Marusina K., Farmer A.A., Rubin G.M., Hoshe P.K.,

A brachenko L., Marusina K., Farmer A.A., Rubin G.M., Hoshe P. S.

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Mallahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Mallahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Mallahy S.J.,

Richards S.A., McEwan P.J., McKernan K.J., Lu X., Gay L.J., Hulyk S.W.,

Richards S.A., Wchey K.C., Hale S., Garcha A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodecgren B.J., Lu X., Gay E.J., Hulyk S.W.,

Richards A. C., Grimwood J., Green B.J., Lu X., Gay E.J., Hulyk S.W.,

Ratesley R.W., Touchman J.W., Green B.D., Lotkeling B.S.,

Rodriguez A.C., Grimwood J., Green B.D., Lotkeling D.S.,

Butterfield Y.S.N., Krzywinski M.I., Skalsku U., Smailus D.S.,

R. Schnerch A., Schehu J.B., Jones S.J.M., Marza M.A.,

Generation and mouse cDNA sequences.",

R. Generation and initial analysis of more than 15,000 full-length

RT Human and mouse cDNA sequences.",

POCO, Natl. Acad. Sci. U.S.A., 99:16899-16903(202).

POCO, Natl. Acad. Sci. U.S.A., 99:16899-16903(202).

POCO, Natl. Acad. Sci. U.S.A., 99:16899-16903(202).

POCO Natl. Also the Ill3 receptors.

PUBCELLULAR LOCATION: Type I membrane protein.

                                                                 STRAIN=CBA/CA;
MEDLINE=53391374; PubMed=8378320;
Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
Cao X., Rozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
(ILD-2R) gamma chain: chromosomal mapping and tissue specificity of ILD-2R gamma chain expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ōĘ
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. REPLANDED 19 PubMed=8359699; Robiling-33666191, PubMed=8359699; Robayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.; Roloning and sequencing of the cDNA encoding a mouse IL-2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95104285; PubMed=7805729;
Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
Fischer A., de Saint Basile G.;
"The murine interleukin-2 receptor gamma chain gene: organization,
chromosomal localization and expression in the adult thymus.";
Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dougherty G.J.; "Molecular mechanisms regulating the hyaluronan binding activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=66341745; Pubmed=8750189;
Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
                                                                                                                                                                                         IL-2R gamma chain expression.";
Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the adhesion protein CD44.";
J. Neurooncol. 26:231-239(1995).
                                                                                                                                                                                                                                                                                                                                                                                             Gene 130:303-304(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
```

```
SECUENCE FROM N.A
                                                        SEQUENCE
                                                                                                                      chain.
   NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                            144 OKLANLONLVIPRAPENLTLSNLSESQLELRWKSRHIKERCLQYLVQYRSNRDRSWTELIV
                                                                                                                                                                                                                                                                                                                                                                                                                                2 NITILIPNGNEDITADFFLITMPIDSLSVSTLPLPEVOCFVFNVEYMNCTWNSSSEPQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMLKLONLVI PWAPENLTLHKLSESOLELNWNNRFL-NHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                        CYTOKINE RECEPTOR COMMON GAMMA CHAIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132 HUMAN STANDARD; PRT; 380 AA.
014627; 000667;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annocation update)
Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13 binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                               Ξ,
                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                 . . .) (POTENTIAL)
. . .) (POTENTIAL)
. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                            66.3%; Score 853.5; DB 1; Length 369; 67.2%; Pred. No. 2.7e-63; ive 33; Mismatches 42; Indels 1
                                                                                                                                                                                                                                                                                                                                                                      CB2D5AB459077AC7 CRC64;
                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                    N-LINKED GLCNAC...) (1
N-LINKED GLCNAC...) (1
N-LINKED GLCNAC...) (1
N-LINKED GLCNAC...) (1
N-LINKED GLCNAC...) (1
N-LINKED GLCNAC...) (1
                                                                                                                                                                                                 InterPro; IPR003531; Hemicopottn_S_Pl.
Pfam; PF00041; fn3; 1.
SMART; SM0066; Fn3; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 22 BY SIMILARITY.
 an email to license@isb-sib.ch)
                                                                                                                                                              MGD; MGI:96551; I12rg.
InterPro; IPR002996; CRIA.
InterPro; IPR003957; FN III-like.
InterPro; IPR003961; FN III-like.
                                                                                         AAB32904.1; JOINED.
AAB32904.1; JOINED.
                                                                                                         S75850; AAB32904.1; JOINED.
S75851; AAB32904.1; JOINED.
X75337; CAA53085.1; -
                                                             AAB32904.1; JOINED
AAB32904.1; JOINED
                                                                                AAB32904.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                           42241 MW;
                                                                                                                                    BC014720; AAH14720.1;
                           U21795; AAA64279.1;
D13565; BAA02760.1;
L20048; AAA39286.1;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                      S75852; AAB32904.1;
                                                                                                                                                I49280; I49280.
                                                                                                                                                                                                                                                                                                                                                         159
164
369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 156; Conserv
                                                             EMBL; S75844;
EMBL; S75845;
                                                                                S75847;
                                                                                                  S75849;
                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
 send
                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                  EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1132 HUMAN
```

g

ਨੇ

g

ል

셤 ਨੇ 셤

ਨ੍ਹ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYMID utstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESUBELLING and Prosence of TISSUBELLING, BIRDARDELE, BOOK NO. RESUBERED AND PROSENCE OF TISSUBELLING, and Prosence of TISSUBELLING, BIRDARDELE, DESCRIPTION OF THE BIRDARDER OF THE SCHOOLE OF THE BIRDARDER OF THE BIRDARDER OF THE BIRDARDER OF THE STANDING OF THE BIRDARDER OF THE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Testis;
Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H.,
Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Brain;
MEDLINE=97321053; PubMed=9177784;
Guo J., Apiou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle (
"Chromosome mapping and expression of the human interleukin-13
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Renal cell carcinoma;
MEDLINE=96279273; PubMed=8663118;
Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N.,
Ferrara P.;
ILI3RA2 OR ILI3R.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitehead S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 271:16921-16926(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor.";
Genomics 42:141-145(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X95302; CAA64617.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
```

```
RL Broc. Natl. Acad. Sci. U.S.A. 99:497-501(1996).

RAGUENCE FROM N.A.

SECURICE FROM N.A.

RAGUENCE FROM N.A.

SECURICE FROM N.A.

RAGUENCE STAINBEATS/; Pubmed-1247793.

RAGUENCE STAINBEATS/; Pubmed-1247793.

RAGUENCE R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Radienko L., Marushar K., Farmer A.A., Rubin G.M., Hong L., Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tochiyaki S. Carninci P., Mullah F., Schaefer C.F., Bhat N.K., Rapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J., Rahas S.A., McEwan P.J., McKernan K.J., Malaman L., McKernan P.J., Makernan R.J., Makernan P.D., Mullahon D.K., Muzny D.M., Sodecgren E.J., Lu X., Gibbs R.A., Villahon D.K., Muzny D.M., Sodecgren E.J., Lu X., Gibbs R.A., Villahon D.K., Muzny D.M., Sodecgren E.J., Lu X., Gibbs R.A., Villahon D.K., Muzny D.M., Godecgren E.J., Lu X., Gibbs R.A., Villahon D.K., Mazny D.M., Godecgren E.J., Lu X., Gibbs R.A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smilus D.E., Butterfield Y.S. N., Krzywinski M.I., Skalaka U., Smilus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences., Towner than 15,000 full-length human and mouse CDNA sequences., Towner CC con form a functional receptor for ILI3. Also serves as an alternate accessory procein to the common cytokine receptor GC con form a functional receptor for ILI3. Also serves as an alternate accessory procein to the common cytokine receptor GC con form a functional receptor for ILI3. Also serves as an alternate accessory procein to the common cytokine receptor GC con form a functional receptor for ILI3. Also serves as an alternate accessory procein to the common cytokine receptor GC con form a functional receptor for ILI3. Also serves as an alternate accessory procein to the common cytokine receptor GC con form a functional receptor for 
                                                                                                                                                                                                                                                                                                                          SO THE THE THE TREE BREEF BREE
MEL; U70981; AAB17170.1; -
EMBL; A027039, AAB17170.1; -
EMBL; A121878; CANDOSO1.1; -
EMBL; A020739, AARDOSO1.1; -
EMBL; A020739, AARDOSO1.1; -
EMBL; A020739, AARDOSO1.1; -
EMBL; B0207739, AARDOSO1.1; -
Genew; HONC:5975, ILILRAD.

M.M. 300130; -
EMBL; B020739, ARILLARD.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0005615; Exinterlewkin receptor activity; TAS.

DR GO; GO:0005615; Finterlewkin receptor activity; TAS.

INTERPORT | FINTERLEWKIN receptor activity; TAS.

THE PROOBSON PROOF ROW IN III.11ke.

THE PROOBSON PROOF ROW IN III.11ke.

THE PROOF ROW III.11ke.

THE PROOF ROW IN III.11ke.

THE PROOF ROW 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 SYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 NLTLHYWYKNSDNDKVOKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPRE--PRRQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 NYNLFYWYEGLDH--ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ATOMIKLONLVIPWAPENLTLHKLSESQLEINWN---NRFLNHCLEHLVOYRTDWDHSWT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 EQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHW-GSNTSKE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 TATVE-NETYTLKTTNETROLCFVVRSKVNIYCSDDGIWSEWSDKOCWEGEDLSKK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1131 MOUSE
009030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID DAT DOT DOT DOT SERVING ON SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
EXTRACELULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                        EMBL; S80963; AAB50695.1; -.
EMBL; BC052425; AAH5939.1; -.
EMBL; BC059939; AAH5939.1; -.
MGJ; MGI:105062; I113ra1.
InterPro; IPR002956; CR1A.
InterPro; IPR003957; FN III-like.
InterPro; IPR003957; FN III-like.
InterPro; IPR003957; FN III-like.
SWART; SW00060; FN III.
PROSITE; PS01356; HEWATOPO REC S F2; I.
Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 N
48402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
26
341
44
132
171
171
103
136
338
424 AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
```

Willson T.A.; "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";

SEQUENCE FROM N.A. MEDLINE=96133964; PubMed=8552669; Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;

Mus musculus (Mouse)

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (ILINRA-1) (Interleukin-13 binding protein) (NR4).

```
6
                                                                                        246 NPQNFRSRCLTYEVEVNNTQTDRHNILEVEEDKCQNSESDRNMEGTSCFQLPGVLADAVY 305
                                                                                                                                         95 LOKKEIHL-YOTFVVOLODPREPRROATOMLKLONLVIPWAPENLTLHKLSESQLELNWN 153
                                                                                                                                                                                                         154 N--RFINHCLEHLVQY---RTD------WDHSWTEQSVDYRHKFSLESVDGGKRY 197
                                                                           94
                                                                     37 EVQCFVFNVEYMNCTWNSSSEPOP-TNLTLHYWYKNSDNDKVQKCSH-YLFSEEITSGCQ
                                                                                                                                                                                                                                                                                                                                                                                                 1131_HUMAN STANDARD; PRT; 427 AA.
PR552; OS9646; O99656;
01-NOV-1997 (Rel. 35, Last sequence update)
15-NAR-2004 (Rel. 31, Last annotation update)
15-NAR-2004 (Rel. 31, Last annotation update)
11-Harleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (IL-13RA OR IL13RA OR IL13RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrara P.;
"Cloning of the human IL-13R alphal chain and reconstitution with the
IL4R alpha of a functional IL-4/IL-13 receptor complex.";
PEBS Lett. 401:163-166(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreas;
MEDINE-22380257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zebberg B., Buetow K.H., Schaefter C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heidel F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURNCE FROM N.A.

TISSUE=B-cell;
Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
Eugster H.P., Bonnefoy J.Y.,
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Carcinoma;
MEDIINE=97165966; PubMed=9013879;
Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA cloning and characterization of the human interleukin 13
   Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Wada M., Hisano T., Kuwano M.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=T-cell;
MEDIINE=97067184; PubMed=8910586;
Aman M.J.; Ayebi N., Obiri N.I., Puri R.K., Modi W.S.,
Leonard W.J.;
     DB 1;
   14.1%; Score 181.5; DB 1 ilarity 27.6%; Pred. No. 8.8e-08; Conservative 38; Mismatches 86
                                                                                                                                                                                                                                                                                                 306 TVRVRVKTNKLCFDDNKLWSDWS 328
                                                                                                                                                                                                                                                                               198 TFRVRSRFNPLC-GSAQHWSEWS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor alpha chain.";
J. Biol. Chem. 271:29265-29270(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
Query Match
Best Local Simil
Matches 56; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              1131_HUMAN
                                                                                                    셤
                                                                                                                                                                                                                                          용
                                                                                                                                                                                                                                                                                                              셤
                                                                       à
                                                                                                                                       ਨੇ
                                                                                                                                                                                                       ጵ
                                                                                                                                                                                                                                                                             ⋩
```

```
DR Genew, HGNC:5974; ILIJakal.

DR Golo005889; C:interleukin-13 receptor complex; TAS.

DR GO; GO:0005889; C:interleukin-13 receptor complex; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.

DR InterPro; IRR00299; CRIA.

DR InterPro; IRR002995; FW_III-like.

DR InterPro; IRR003957; FW_III-like.

DR InterPro; IRR003957; FW_III-like.

DR InterPro; IRR003957; FW_III-like.

DR InterPro; IRR0039532; Hemtopoptn S.F2.

TRANSMAL 1 POTENTIAL.

FT CHAIN 22 427 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.

FT CHAIN 34 367 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 348 427 CYTOPLASMIC (POTENTIAL).

POWAIN 46 95 POTENTIAL.
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Rahary D.M., Sodergren B.J., Lu X., Gay L.J., Hulyk S.W., Rahary D.M., Sodergren B.J., Lu X., Gabbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Rahakesley R.W., Touchman J. W., Green B.D., Dickson M.C., Rahakesley R.W., Touchman J. W., Green B.D., Dickson M.C., Rahakesley R.W., Touchman J. W., Green B.D., Myers R.W., Touchman J. W., Green B.D., Myers R.W., Rodriguez A. C., Grimwood J., Schmutz J., Myers R.W., Touchman J. W., Green B.D., Myers R.W., Touchman J. W., Green B.D., Myers R.W., Touchman J.W., Green B.D., Myers R.W., Marra M.A., Schein J.S.A., Schein J.S.A., Marra M.A., Fenceration and initial analysis of more than 15,000 full-length run form a functional receptor for ILL3. Also serves as an alternate accessory protein to the common cytokine receptor gamma chain for IL4 signaling with cannot replace the function of gamma chain for IL4 signaling but cannot replace the function of gamma chain for IL4 signaling with cannot replace the function of gamma chain general muscle and ovary; lowest levels in brain, lung and kidney. Also found in B-cells, T-cells and endothelial cells.

- INSUMERATIY: Belongs to the type I cytokine family of receptors. Subfamily S.
- BATABASE: NAME=PROW; NOTE=PROW 2:95-100(2001);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
T -> T (TW PER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y10659; CAA71669.1; -.
EMBL; Y09328; CAA70508.1; -.
EMBL; U628885; AAB37127.1; -.
EMBL; U81379; AAD00510.3; -.
EMBL; BC009960; AAH09960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
```

Φ

us-09-825-561a-4.rsp

```
CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                         ----
  ------EQSVDYRHKFSLP 189
                                                                                                                                                                                                                                                                                                                                 245 VQWENPQNFISRCL----FYEVEVBVNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP 300
                                                                                                                                                                                                                           QLQXKKEIHLYQTFVVQL--QDPREPRRQATQMLKLONLVIPWAP--ENLTLHKLSESQLE 149
                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIŜSUE-Lung;
Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
                                                                                                                                             EVOCEVENVEYMNCTWNSSSEPOP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21311890; PubMed=11418668;
MEDLINE=21311890; PubMed=11418668;
Reche P.A., Soumelis V., Gorman D.M., Clifford T., Liu M.-R.,
Travis M., Zurawski S.M., Johnston J., Liu Y.-J., Spits H.,
de Waal Malefyt R., Kastelein R.A., Bazan J.F.;
"Human thymic stromal lymphopoletin preferentially stimulates myeloid
                                                                                                                                                                                                                                                     TISSUE=T-cell;
MEDLINE=21367592; PubMed=11474172;
TONORUKA Y., Fujio K., Sugiyama T., Nosaka T., Hirai M., Kitamura T.;
"Molecular cloning of a human novel type I cytokine receptor related
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRLZ HUMAN STANDARD; PRT; 371 AA.

O9HC73; Q9H5R3;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cytokine receptor-like factor 2 precursor (Cytokine receptor-like (CRLE2) (IL-XR) (Thymic stromal lymphopoietin protein receptor)
(TSLPR).
(CRLF2X OR CRLF2 OR ILXR) AND (CRLF2Y OR CRLF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a novel type I cytokine receptor CRL2 preferentially expressed by human dendritic cells and activated
                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Dendritic cell;
MEDLINE=21134329; PubMed=11237741;
MEDLINE=21184329; PubMed=1237741;
Zhang W., Wang J., Wang Q., Chen G., Zhang J., Chen T., Wan
                                                          Length 427;
                                                                                                   83; Indels
358 G -> D (IN REF. 3).
48759 MW; 5983B3E8F554107B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       190 SVDGOKRYTFRVRSRFNPLC-GSAQHWSEWSHPIHWG 225
                                                                                                                                                                                                                                                                                                                                                                                                                 GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 281:878-883(2001).
                                                        13.8%; Score 178; DB 1;
llarity 26.7%; Pred. No. 1.7e-07;
Conservative 38; Mismatches 83;
                                                                                                                                                                                                                                                                                                           150 INWNN--RFLNHCLEHLVQYRTDWDHSWT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to deltal/TSLPR.";
Cytogenet. Cell Genet. 93:23-25(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunol. 167:336-343(2001).
    358
427 AA;
                                                                            Local Similarity
nes 58; Conserv
    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                            Query Match
                                                                                                                                             37
                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
CRL2 HUMAN
                                                                                    Best Loca
Matches
      SOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PACA REPARE TO THE REPARCE OF THE PACE OF 
                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                         ਨੇ
                                                                                                                                                                                  셤
                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                  쉽
                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                            쉼
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SKOENTCNVTIEGLDAEKCYSFWYRVKAMEDVYGPDTYPED WESVTCWGRESBIRDACAFPTPPREKLEKET. -> TGSRSV TOACVGWCDLCLLOESPBREKRFSCLELESSWDYHPPPRE.
ANFCIISRDGVSFCWPGWSRTCDLR (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and call-surface receptor binding.
-1- DOMAIN: The BOX 1 motif is important for association with JAKs.
-1- SIMILARITY: Belongs to the type I cytokine family of receptors.
-1- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; Leacondong 1...
SMART, SMORGOG, FIL, FALSE NEG.
PROSITE; PSO1355; HEMATOPO REC S FI, FALSE NEG.
Receptor; Signal; Transmembrane; Glycoprotein; Alternative splicing.
SIGNAL 1 22 POTENTIAL.
CHAIN 23 371 CYTOKINE RECEPTOR-LIKE FACTOR 2.
CHAIN 23 231 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INOTICE OF THE PROPERTY OF THE
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
WEXWS MOTIF.
BOX 1 MOTIF.
BY SIMILARITY.
N-LINKED (GLCMAC. . . ) (PO
N-LINKED (GLCMAC. . . ) (PO
N-LINKED (GLCMAC. . . ) (PO
N-LINKED (GLCMAC. . ) (PO
N-LINKED (GLCMAC. . . ) (PO
N-LINKED (GLCMAC. . . ) (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP 008787.
MISSING (IN REF. 4).
DEA53814758B69E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (In isoform 2) P 008787.
                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTId=VSP 008786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1;
IsoId=Q9HC73-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000282; Cytok receptor_2.
Interpro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF142570; AAG27923.1; -.
EMBL; AB055639; BAB60717.1; -.
EMBL; AR338733, AAK6618.1; -.
EMBL; AK02680; BAB15557.1; -.
Genew; HGNC.14281; CRLF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
42012 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
233
233
233
200
261
71
71
47
47
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
```

```
Cell 104:291-300(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISULFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
        88 AEQRDDILYFSIRNGTHPVFTASRWAYYLKPSSPK------HVRFSWHQDAVTV- 136
                                                                                                                                                                       -OKKEIHLY-------QTFVVQLQDPREPRQATOMLKLQNLVIPWAPENLTLH 141
                                                         9
2
                                                                    31 QIQIIYENLETVQVTWNASKYSR-TNLFFFYRF-NGD-EAYDQCTNYLLQEGHTSGCLLD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 338-438.
MEDILIPAS20219736; PubMed=10753826;
ROBSJOHN J., MCKINBLYY WOOGGOCK J.M., MCClure B.J., Hercus T.R.,
Parker M.W., Lopez A.F., Bagley C.J.;
"Structure of the activation domain of the GM-CSF/IL-3/IL-5 receptor
common beta-chain bound to an antagonist.";
                                                     37 EVQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSREITSGCQL-
                                                                                                                                                       142 KLSESQLEINWINRFINHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 338-438.

MEDLINE=20202378; PubMed=10736232;

Mulhern T.D., Lopez A.F., D'Andrea R.J., Gaunt C., Vandeleur L.,
Vadas M.A., Booker G.W., Bagley C.J.;

"The solution structure of the cytokine-binding domain of the common beta-chain of the receptors for granulocyte-macrophage
colony-stimulating factor, interleukin-3 and interleukin-5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21124834; PubMed=11207369;
Carr P.D., Gustin S.E., Church A.P., Murphy J.M., Ford S.C.,
Mann D.A., Woltring D.M., Walker I., Ollis D.L., Young I.G.;
"Structure of the complete extracellular domain of the common beta
subunit of the human GM-CSF, IL-3, and IL-5 receptors reveals a novel
dimer configuration.";
                                  Gapa
                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (Rel. 27, Created)
01-PEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
CSP/ZIL-3 receptor common beta chain precursor (CDw131 antigen) (GM-CSP/ZIL-3/IL-5 receptor common beta-chain).
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
                                41;
     Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-91088571; PubMed-1702217;
Hayashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of a second subunit of the receptor for granulocyte-macrophage colony-stimulating factor (GM-CSF): reconstitution of a high-affinity GM-GSF receptor.", proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kitamura T.;
Submitted (FEB-1991) to the EMBL/GenBank/DDBJ databases.
                                70;
     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 25-437.
  12.4%; Score 159.5; DB 1
25.0%; Pred. No. 4.9e-06;
ive 42; Mismatches 70
                                                                                                                                                                                                                                                                                                    897 A.A.
                                                                                                                                                                                                                                  RVKAMEDVYGPDTYPSDWSEVTCW 209
                                                                                                                                                                                                           RSR-FNPLCGSAQHWSEWSHPIHW 224
Query Match
Best Local Similarity 25.0%
Matches 51, Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISION TO 454.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                           202
                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                      CYRB HUMAN
                                                     ò
                                                                                                                             d
                                                                            셤
                                                                                                      ઠે
                                                                                                                                                        ઠે
                                                                                                                                                                                                         ਨੇ
```

SEQUENCE

VARIANT

94

셤 ò

à

à 엄 à g

us-09-825-561a-4.rsp

```
PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Mismatches
                                                                                                                                                                BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                    N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                 N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=94193800; PubMed=8144676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 RFNPLCGSAQHWSEWSHPIH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 TLDP----GEWSEWSSERH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                           94102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                               / Mac.
Local Sim.
50; C
                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                DOMAIN
DISULFID
DISULFID
SIGNAL
CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                   OMAIN
                                                                           OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                         OLOKKETHLYOTFVVOLODPREPRROATOMIKLONLVIPWAPENLTLHKLSESOLELNWN 153
                                                                                                                                                                          154 NRFLNHCLEHL-----VQYRTD---WDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                    38 VOCEVENVEYMNCTWNSSSEPOPTNLTLHYWYKNSDNDKVOKCS----HYLFSEELTSGC
                                                                                                                   34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=White leghorn; TISSUB=Kidney;
MEDLINE=93075121; PubMed=1445292;
Tanaka M., Maeda K., Okubo T., Nakashima K.;
"Double antenna structure of chicken prolactin receptor deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the CDNA sequence.";
Biochem. Biophys. Res. Commun. 188:490-496(1992).
-!- FUNCTION: This is a receptor for the anterior pituitary hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prolactin.
SUBCELULAR LOCATION: Type I membrane protein.
SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 1.
                                                                           Length 897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, D13154; BAA02439.1; -...
PIR; JQ1655; JQ1655.
HSSP, P16471; 1BP3.
InterPro; IPR00296; CRIA.
InterPro; IPR003961; FN III-like.
InterPro; IPR003961; FN III-like.
InterPro; IPR003528; Hemtopoptn_L.F1.
Pfam; PF00041; fn3; 4.
SWART; SW00060; FN3; 3.
PROSITE; P201352; HEMATOPO_REC_L.F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
                                                                             Query Match 12.3%; Score 159; DB 1; Length 89
Best Local Similarity 26.4%; Pred. No. 1.6e-05;
Matches 55; Conservative 40; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subfamily 1.
-!- SIMILARITY: Contains 4 fibronectin type III domains.
       V -> M (in dbsNP:1801114)
                         /FTId=VAR 014803.
3398E37FDB8F393A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Prolactin receptor precursor (PRL-R) (CPRLP).
                                                                                                                                                                                                                                                                                                                                                                                                                   417 SRIGYNGI -----WSEWSEARSWDTES 438
                                                                                                                                                                                                                                                                                                                                                                               ---- FNPLCGSAQHWSEWSHPIHWGSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                           897 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
       652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHICK
```

004594;

```
151 --NWNNRFL----NHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 WAKWSPPLLADASSNHLYHYELRIKDEEKEEWETISVGVQTQCKINRLNAGMRYVVQVRC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 IRCRSLEKETFSCWWKPGSDGGLPTNYTL--FYSKDSEBEIYECPDYR-----TSGPNSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 YFNKNHTSPWITFNITVIAINEIGSNSSDPQYVDVTSIVQPGSPVNLTLETKRSANIMYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 OLOKKEIHLYQTFVVQLODPREPRRQAT--QMLKLQNLVIPWAPENLTLH-KLSESQLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 VOCFVFNVEYMNCTWNSSSE-POPTNLTLHYWYKNSDNDKVQKCSHYLFSEELTSG---C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Placenta;
MEDLINE-90059966; PubMed=2555171;
Gearing D.P., King J.A., Gough N.M., Nicola N.A.;
Expression cloning oct a receptor for human granulocyte-macrophage colony-stimulating factor.";
EMBO J. 8:3667-3676(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi.
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACK HUMAN STANDARD; PRT; 400 AA.
PISSO9, 000207, Q14429; Q14431; Q16564;
01-ARR-1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Granulocyte-macrophage colony-stimulating factor receptor alpha chain precursor (GM-CSF-Ralpha) (GMR) (CDW16) (CD116 antigen).
(CSF2RAX OR CSF2RA OR CSF2R OR CSF2RX) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa Y., Kosugi H., Miyajima A., Arai K.-I., Yokota T.; "Structure of the gene encoding the alpha subunit of the human granulocyte-macrophage colony stimulating factor receptor. Implications for the evolution of the cytokine receptor
                                                                                                                                                                                                                                                                                                                                     POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.6%; Score 150; DB 1; Length 831; 25.0%; Pred. No. 7.9e-05;
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1C4E75791DCADBE9 CRC64;
                                                                                     FIBRONECTIN TYPE-III 1. PIBRONECTIN TYPE-III 2. PIBRONECTIN TYPE-III 3. PIBRONECTIN TYPE-III 4.
                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                          (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC
```

```
BECONSIGNATION OF THE STATE OF
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRANULOCYTE-MACROPHAGE COLONY-STIMULATING 
FACTOR RECEPTOR ALPHA CHAIN, 
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                Isold-P15509-6; Sequence-VSP 001663, VSP 001664; SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                         IsoId=P15509-3; Sequence=VSP_001668, VSP_001669;
                                                                                                                Name=4;
IsoId=P15509-4; Sequence=VSP_001665, VSP_001666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (PN-LINKED (GLCNAC. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM) 4250U01,

GO, GO:0006887; C:integral to plasma membrane;

GO, GO:0004872; F:receptor activity; TAS.

InterPro; IPR00296; CRIA.

InterPro; IPR003961; FN III-like.

InterPro; IPR003961; FN III-like.

InterPro; IPR003951; Hemtopoptn S-F2.

PROSITE; PS01356; HEMATOPO_REC_S-F2; 1.
                      Name=2;
IsoId=P15509-2; Sequence=VSP_001670;
                                                                                                                                                                                        IsoId=P15509-5; Sequence=VSP_001667;
  IsoId=P15509-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X17648, CAA35638.17

EMBL, D26618, BAA05656.17

EMBL, D26619, BAA05656.17

EMBL, D26619, BAA05656.17

EMBL, D26620, BAA05656.17

EMBL, D26621, BAA05656.17

EMBL, D26621, BAA05656.17

EMBL, D26621, BAA05656.17

EMBL, D26622, BAA05656.17

EMBL, D26624, BAA05656.17

EMBL, D26625, BAA05656.17

EMBL, D26626, BAA05656.17

EMBL, D26626, BAA05656.17

EMBL, D26627, BAA05656.17

EMBL, D26627, BAA05656.17

EMBL, S4455, CAA35908.17

EMBL, S4455, CAA35908.17

EMBL, 129348, AAA60962.17

EMBL, 129348, AAA60962.17

EMBL, 129348, AAA60962.17

EMBL, 129348, AAA60962.17

EMBL, B29349, AAA60962.17

EMBL, B29349, AAA60962.17

EMBL, B29349, AAA60962.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; 806945; 806945.
PIR; 813684; 813664.
PIR; 850039; 850040.
PIR; 850040; 850040.
Genew; HGNC; 2435; CSF2RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400
400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 306250; -.
MIM; 425000; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; 1
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAIN
```

```
94394 MW; 220916320F77FAC1
                                     SEQUENCE OF 82-121 AND 473-522 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO02957; FN III-like.
InterPro; IPRO03951; FN III.
InterPro; IPRO03501; FN III.
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 3.
Biol. Reprod. 55:1081-1090(1996)
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 176587; AAB01544.1; -. EMBL; U22947; AAA75038.1; -. EMBL; U22924; AAA75039.1; -. HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                interPro; IPR002996; CRIA.
InterPro; IPR008957; FN II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
   SO THE SELECT STATES THE SELECT SERVICE SECOND SELECT SELECT SERVICES SO THE SERVICES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KKEIHLYQTFV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                         GSDGGLGS_VIYVL_IVGTLVCGIVLGFLFKRFLRIQRLF
PPVPQIKDKLADNHBVEDEIIWEEFTPEEGKGYREEVLTVK
EIT -> DDHLGGIHPRGRERLPRRGLDREGNYLRPRGCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                -- MGPQRHHRCGWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S ILTPN-GNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNL
                                                                                                                                                                                                                                                                                               GMDISASATRGNCFLDDAVNLYIIFYVFI (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 LLYPNSGREGTAAQNF-----SCFIYNADLMNCTW-ARGFTAPRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 VQLQDPRE----PRRQATQMIKLQNLVIPWAPENLTLHKLS--ESQLELNWNNRFLNHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OYFLYIRNSKRRRIRCPYYIQDSGTHVGCHLDNLSGLTSRNYFLVNGTSRRIGI--QFF
                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
ERFNPPSNVIVRCNTIHC -> GSLGYSGCSRQFHRSKIN
                                                                                                                                                                                                                                                                                                                                     /FTId=VSP_001667.
DDGNLGSVXIYVLLIV -> LGYSGCSRQFHRSKTN (in
                                                                                                                                                INVSGDLENRYNFPSS -> VVLTTGTSALCTFMCS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Kidney;
MEDLINE=97057891; PubMed=8902221;
MEDLINE=97057891; PubMed=8902221;
MeDLGIT acloning tissue distribution, and expression of the prolactin receptor during various reproductive states in Meleagris gallopavo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meleagris gallopavo (Common turkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria; Aves; Neognathae, Galliformes; Phasianidae, Meleagris.
NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYPTPGPSPGSGSSPRLGSESSL (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                          dissing (in isoform 3).
FIId=VSP 001669.
                                                                                                                                                                                                        (In isoform 4).
                                                                             (in isoform 6).
/FTId=VSP 001663.
Missing (in isoform 6)
/FTId=VSP_001664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 6.3e-05; 44; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                001668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 TLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91034; Q91091; Q91092;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NAR-2004 (Rel. 43, Last annotation update)
Prolactin receptor precursor (PRL-R) (TPRLR).
                                                                                                                                                                                        001665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   831 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 146.5;
                                                                                                                                                                                    FTId=VSP
                                                                                                                                                                                                                            FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                              Boform 3)
                                                                                                                                                                                                                                                                                                                                                                                              FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                    Missing
                                                                                                                 Missing
                                                                                                                                                                                                            Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.4%; 21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
   229
272
305
233
                                                                                                                                                  286
                                                                                                                                                                                                                                             400
                                                                                                                                                                                                                                                                                                                                                                                                                400
                                                                                                                                                                                                                                                                                                                                                                                                                                                      400
                                                                                                                 400
                                                                                                                                                                                                          400
                                                                                                                                                                                                                                                                                                                                                          333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 AIEFGSD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIHWGSN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                334
                                                                                                                                                                                                                                                                                                                                                                                                                                                    376
   229
272
305
216
                                                                                                                  234
                                                                                                                                                                                                            287
                                                                                                                                                  271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
   CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                 VARSPLIC
                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 KCSHYLFSEBITSG---CQLQKKBIHLYQTFVVQLQDPREPRRQAT--QMLKLQNLVIPW 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 APENLTLHKLSESQLELN-----WNNRFL-----NHCLEHLVQYRTDWDHSWTEQSVD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 BCPDYR ----TSGPNSCYFNRNYTNSWTTYRITYTATNEIGSNSSDPQYVDVTSIVQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSE-PQPINLTLHYWYKNSDNDKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 11.3%; Score 145.5; DB 1; Length 831; L Similarity 24.3%; Pred. No. 0.00018; Si, Indels 35; Gaps 53; Conservative 36; Migmatches 94; Indels 35; Gaps
TISSUR=Ovary;
Patts G.R., You S.K., Foster D.N., el Halawani M.E.;
Submitted (MAR-1995) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: This is a receptor for the anterior pituitary hormone
                                                                                                                                          prolactin.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SIMILARITY: Belongs to the type I cytokine family of receptors.
--- Subfamily 1.
--- SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ( POTENTIAL)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
PIBRONECTIN TYPE-III 1
PIBRONECTIN TYPE-III 2.
PIBRONECTIN TYPE-III 4.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ...) (P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTE; PS0135; HEWATOPO REC L F1; 1.
PROSTE; PS0135; HEWATOPO REC L F1; 1.
SIGNAL 1 23 POTENTIAL.
CHAIN 24 831 PROLACTIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 YRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWS 219
```

g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      Chen X., Horseman N.D.; "Cloning, expression, and mutational analysis of the pigeon prolactin receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrinology 135:269-276(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors
                                                                                                                                                                                                                                                       Columba livia (Domestic pigeon).
Wararyota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba,
NCBI_TaxID=8932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 132.5; DB 1; Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U07694; AAA20646.1; -...
PTR; IS0455; I50455.
HSSP; PIG471; 1BR3.
InterPro; IPR00895; FN III-like.
InterPro; IPR00895; FN III-like.
InterPro; IPR003528; Hemtopoptn_L.F1.
PROSUTE; SM00060; FN3; 4.
PROSITE; PS01252; HEMATOPO REC_L.F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactin.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Subfamily 1.
SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3B074E83CDF69EFF CRC64;
185 VQTQCKINRLNAGMRYVVQVRCMLDP----GEWSEWS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC.
                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prolactin receptor precursor (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC
                                                                                                              830 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Cropsac;
MEDLINE=94283267; PubMed=7516866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94507 MW;
                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336
830 AA;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                             RESULT 13
PRLR COLLI
ID PRLR COLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
```

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                         90 KNHINPWITYNIIVWAMNEIGSNSSDPQYVDVISIVQPDAPVNLSLETKISASITYLLAK 149
                                                                                                                                                                                                                                                     |: : : : : : | :| | 150 WSPPPLADVTSNSHVRYBELEREKEEWETVSVGVQTQYKVNRLQAGVKYVVQVRCVL 209
                                                                                                                                                 97 KKEIHLYQTFVVQLQDPREPRRQAT--QMLKLQNLVIPWAPENLTLH---KLSESQLELN 151
                                                                                                                                                                                                                              152 WNNRFL-----NHCLEHLVOYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRF 205
                                                                   38 VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ 96
                                                                                                   34 IRCRSLEKETPSCWWKPGSDGGLPTNYTL--PYSKDSEEKIYECPDYGMSG--PNSCYFD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-STORM K.M. PLONGAR 18 MEDLINE-SOLUTION NO. MEDLINE-STORM NO. MINDLINE-SOLUTION NO. Castle B.E., Gorman D.M., Itoh N., Schreurs J., Hardad N., Castle B.E., Gorman D.M., Itoh N., Schreurs J., Barrett R.L., Howard M., Miyalima A.; Expression cloning of a cDNA encoding the murine interleukin 4 receptor based on liqand binding.";

1. FUNCTION: This is a receptor for interleukin-4. The soluble form of the IL4 receptor may respressnt a regulatory molecule specific for II4-dependent immune responses.

1. SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.

1. SUBUNIT: Heterodimer of an alpha chain and secreted.

1. ALTERNATIVE PRODUCTS:

EVent-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE SEQUENCE FROM N.A., SEQUENCE OF 26-39; 162-179 AND 194-210, AND ALTERNATIVE SPLICTING.

MEDIINE-90030408; PubMed=2805066;

MOSILY B., Beckmann M.P., March C.J., Idzerda R.L., Gimpel S.D., Vanden Bos T., Friend D., Alpert A., Anderson D., Jackson J., Vanden Bos T., Friend D., Alpert A., Anderson D., Uackson J., Cosman D., Park L.S.,

"The murine interleukin-4 receptor: molecular cloning and characterization of secreted and membrane bound forms";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold=P16382-3; Sequence=VSP_001677;
Note=Lacks the cytoplasmic domain. Binds IL-4;
SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
15-WAR-2004 (Rel. 43, Last ambotation update)
Interleukin-4 receptor alpha chain precursor (IL-4R-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=2; Synonyms=secreted;
IsoId=P16382-2; Sequence=VSP_001675, VSP_001676;
0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
          22.2%; Pred. No. 0.00
cive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1; Synonyms=Membrane;
Isold=P16382-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                          206 NPLCGSAQHWSEWSHPIH 223
                                                                                                                                                                                                                                                                                                                                       :
210 D----IGEWSEWSSERH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A. (ISOFORM 1)
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note=Binds IL-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note=Binds IL-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL4R OR IL4RA.
Mus musculus (Mouse)
        Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subfamily 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                               IL4R MOUSE
P16382;
                                                                                                                                                                                                                                                                                                                                                                                                                          IL4R_MOUSE
                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ્ઠ
                                                                                                                                               ઠે
                                                                                                                                                                                   셤
                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                           셤
```

```
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 -----RLMFPEPSENLTCIPRNSASTVCVCHMEMNRPVQSDRYQMELWAEHRQLWQGSF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 KLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCL--EHLVQY----RTDWDHSWTEQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 SPSGNVKPLAPDNITIHTNVSDEWILTWANLYPSNNLLYKDLISMVNISREDNPAEFIVY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 TTADFFLITMPTDSLSVSTLPLPEVQCFVFNVBYMNCTW-NSSSEPQPTNLTLHYWYKNS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 DNDKVQKCSHYLFSEBIT-----SGCQLQKKEIHLYQTFVVQLQDPREPRQATQML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ISVGCLILLLVIGSGSIKVLGEP--ICRSDYIRTSTCEWFLDSAVDCSSQLCLHY----
                                                                              EMBL; M27959; AAA39299.1; --
EMBL; M27960; AAA39300.1; --
EMBL; M27964; AAA39300.1; --
EMBL; M23964; AAA39300.1; --
EMBL; M33380, AAA39300.1; --
EMBL; M33380, A3380, A3380
MGD; MGI:105367; Il4ra.
InterPro; IPR002966; CRIA.
InterPro; IPR003961; FW_III.
InterPro; IPR003961; FW_III.
SMART; SM00060; FN3; 1.
RECEPTOR PROMOSO, FN3; 1.
RECEPTOR TANNERSE S. HEMATORO REC S. F1; 1.
RECEPTOR: Transmembrane; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CDw131 antigen) (GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last amotation update)
15-MAR-2004 (Rel. 43, Last amotation update)
Cytokine receptor common beta-chain)
CSF/IL-3/IL-5 receptor common beta-chain).
Mus musculus (Mouse).

Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                            POLY-GLU:
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .)
                                                                                                                                                                                                                                    INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVDY---RHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 NVTYKEPRLSFPINILMSGVYYTARVRVRSQILTGT---WSEWSPSITW 222
                                                                                                                                                                                                                                                                                                                                                                             HPOLPL -> PSNENL (in isoform 2)./FIId=VSP_001675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 132; DB 1; Length 810; 26.2%; Pred. No. 0.0023; ive 28; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (In isoform 3).
/FTId=VSP 001677.
536B9E0IE938FF6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Missing (In isoform 2). /FIId=VSP_001676.
                                                                                                                                                                                                                                                                                                                                                                                                                           (In isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     810 AA; 87627 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              258
                                                                                                                                                                                                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYRB MOUSE
P26955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                        /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                              /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
CYRE MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OC GE DE DE DE
             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
SECURISE SOLUTION NA.

REPLIKES 9013911 PubMed169379;
REPLIKES 9013911 PubMed169379;
REPLIKES 9013911 PubMed169379;
REPLIKES 9013911 PubMed169379;
REPLIKES 901391 PubMed189379;
REPLIKES
```

qq

412 YCARVRVK--PISNYDGIWSKWSEEYTW 437

Search completed: March 3, 2004, 12:36:12 Job time : 9.71896 secs

Sequence 12, Appl Sequence 72, Appl Sequence 78, Appl Sequence 78, Appl Sequence 66, Appl Sequence 66, Appl Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 68, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 36, Appli Sequence 7, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 26, Appli Sequence 56, Appli

853.5 66.3 369 9 215 16.7 561 9 215 16.7 561 9 215 16.7 561 9 215 16.7 563 9 213 16.5 318 9	213 16.5 386 9 207 16.1 317 9 207 16.1 380 9 207 16.1 380 9	207 16.1 380 17. 200 16.0 205 9 200 16.0 205 9 200 16.0 205 9 200 16.0 205 9 200 16.0 200 16.	25.5 14.2 3/2 10 US-03-090-08-08-181 14.1 776 14 US-10-287-0 181 14.1 776 14 US-10-287-0 181 14.1 776 14 US-10-287-0 14.0 426 13 US-10-036-1 179 13.9 778 9 US-09-935-86 179 13.9 778 14 US-10-35-86-1 179 13.9 778 14 US-10-287-0 179 13.9 778 14 US-10-287-0	179 13.9 778 14 US-10 179 13.9 778 14 US-10	RESULT 1 US-09-825-561A-4 IS-09-825-561A-4 Sequence 4, Application US/09825561A Sequence 4, Deplication US/09825561A Sequence 6, Application US/09825561A Sequence 700-8020020137677A1 APPLICANT: West, James W. APPLICANT: West, James W. APPLICANT: Presnell, Scott R APPLICANT: Holly, Richard D. APPLICANT: Nelson, Andrew J. TITLE OF INVENTION SOLUBLE ZALPHAII CYTOKINE RECEP FILE OF INVENTION SOLUBLE ZALPHAII CYTOKINE RECEP	CURRENT APPLICATION NUMBER: US/09/825,561A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US/0/194,731 PRIOR FILING DATE: 2000-04-05 PRIOR PILING DATE: 2000-07-08 NUMBER OF SEQ ID NOS: 86 SEQ ID-NOS: PARESEQ FOR WINDOWN VERSION 3:0	LENGTH: 232 TYPE: PRT TY
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on: Maxch 3, 2004, 12:38:15 ; Search time 30.3268 Seconds	(without alignments) 1615.322 Million cell updates/sec Title: US-09-825-561A-4 Perfect score: 1288 Sequence: 1 LATTILTPNGNEDITADPFLOHWSEWSHPIHWGSNTSKEN 232	ng table: BLOSUM62 Gapop 10.0 , Gapext 0.5 ned: 809742 seqs, 211153259 residues	Total number of hits satisfying chosen parameters: 809742 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Jatabase: Published Applications AA:* 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:* 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:* 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:* 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:* 5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*	6: /cgn2_6/ptodata/1/pubpaa/PCTUS PUBCOMB.pep:* 7: /cgn2_6/ptodata/1/pubpaa/USOB_XEW_PUB.pep:* 8: /cgn2_6/ptodata/1/pubpaa/USOB_XEW_PUB.pep:* 9: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 10: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 11: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 12: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 13: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 14: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 15: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 16: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:* 17: /cgn2_6/ptodata/1/pubpaa/USOB_WEW_PUB.pep:* 18: /cgn2_6/ptodata/1/pubpaa/USOB_WEW_PUB.pep:* 18: /cgn2_6/ptodata/1/pubpaa/USOB_WEW_PUB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Seault Ouery No. Score Match Length DB ID	1288 100.0 232 9 100.0 232 561A-4 Sequence 4, Appli 2 1288 100.0 369 15 100.0 369 15 100.0 369 15 100.0 369 15 100.0 369 15 100.0 369 15 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 100.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 16 160.0 369 3

45

LPHA11 CYTOKINE RECEPTORS

CSHYLKSERITSGCQLQKKRIHLYQTFVVQLQDPREPRRQA 120

LTTMPTDSLSVSTLPLPEVQCFVFNVBYMNCTWNSSSEPQP 60. LITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP

Gaps

ö

Score 1288; DB 9; Length 232; Pred. No. 1.3e-119; Mismatches 0; Indels 0;

```
Query Match
Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-20
                                                                                                                                                               ; ORGANISM: Rat
US-10-116-275-339
                                                                                                                                                                                                                              Query Match
Best Local S
Matches 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 339, Application US/10116275
Sequence 339, Application US/10116275
Sequence 339, Application US/10116275
Sublication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Downer, David
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Inala
APPLICANT: Higgins, Lisa
IITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
180
                             TOMIKLONIVIPWAPENLTIHKUSESQIEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNLTLHYWYKNSDNDKVQKCSHYLFSEBITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRPLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOMIKLONLVI PWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 INTILITPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVSYNCTWNSSSEPQP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 INTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: soluble human IL-2Rgamma/human kappa light chain
CHER INFORMATION: polypeptide
US-09-825-561A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                   DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                               181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
                                                                                                                                                                                                                                                                                       APPLICANT: STEELER, Cindy A. APPLICANT: SPECIEL, Cindy A. APPLICANT: SPECIEL, Cindy A. APPLICANT: No. US20020137677Alak, Julia E. APPLICANT: No. US20020137677Alak, Julia E. APPLICANT: Presnall, Scott R. APPLICANT: Holly, Richard D. APPLICANT: Holly, Richard D. APPLICANT: Hollon, Andrew J. TITLE OF INVENTION: SOLUBLE ZALPHAII CYTOXINE RECEPTORS FILE REPRESENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT PILING DATE: 2000-04-05
PRIOR PELICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
NUMBER OF FULING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FASTERQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1288; DB 9;
Best Local Similarity 100.0%; Fred. No. 2.3e-118;
Matches 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              Sequence 18, Application US/0982551A Patent No. US20020137677A1
                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-116-275-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
121
                                      121
                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                             g
                                                                                                                      유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
ò
                                                                                 ઠે
```

```
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
SEQ ID NO 339
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 INLTILHYWYKUSDNDKVOKCSHYLFSEEITSGCOLOKKEIHLYQTFVVOLODPREPRROA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TOMIKLONIVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 TOMIKLONIVIPWAPENITLHKLSESQLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNLTLHYWYKNSDNDKVQKCSHYLPSBEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 INLILHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOMIKLONIVIPWAPENLILHKUSESQLELNWNNRPLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 TOMIKLONLVIPWAPENLTIHKUSESOLELNWANNRFLAHCLEHLVOYRTDWDHSWTEOSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09935868
Sequence 20, Application US/09935868
Patent No. US20020164690A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and I
FILE REPERENCE: REG 203D
FILE REPERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN Version 3.0
IENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 TNLTLHYWYKNSDNDKVQKCSHYLFSEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 INTILITYPUGNEDTTADFFLTTMPTDSLSVSTLFLFEVQCFVFNVEYMNCTWNSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 INTIILTPNGNEDITADFFLITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                              tch 100.0%; Score 1288; DB 15; Length 369; al Similarity 100.0%; Pred. No. 2.4e-118; 232; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1288; DB 9; 100.0%; Pred. No. 5,4e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
```

```
US-09-935-868-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-935-868-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      පු පු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TNLTLHYWYKNSDNDKYQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOMIKLONLVIPWAPENLILHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 INLILHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 TOMIKLONIVIPWAPENLTLHKISESQLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV 202
Sequence 20, Application US/10287035
Publication No. US20030104567A1
GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REPERENCE: REG 203DA
CURRENT APPLICATION NUMBER: US/10/287,035
CURRENT APPLICATION NUMBER: USS/005-11-01
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-03-22
PRIOR PILING DATE: 1990-05-19
PRIOR PILING DATE: 1990-05-19
PRIOR PILING DATE: 1999-05-19
PRIOR PILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 20
LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-B-US
CURRENT PILING DATE: 1099-09-22
PRIOR PILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PRECEPTOR Windows Version 3.0
SEQ ID NO 20
LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LNTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 INTILLTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYRHKRSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1288; DB 14;
100.0%; Pred. No. 5.4e-118;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
S-10-287-035-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
S-10-282-162-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-282-162-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
```

```
Sequence 18, Application US/09935868
Patent No. US20020164690A1
Fatent No. US20020164690A1
FAPPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using FILE REFERENCE: REG 2013D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
FALOR PAPLICATION NUMBER: PCT/US99/22045
RANDR PAPLICATION NUMBER: PCT/US99/22045
RANDR PAPLICATION NUMBER: PCT/US99/22045
RANDR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 18
LENGTH: 694
                                                                                                                                                                                                                                                                                                                                                       83 TNLTLHYWYKNSDNDKVQKCSHYLPSBRITSGCQLQKKRIHLYQTFVVQLQDPRBPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 INLILHYWYKNSDNDKVOKCSHYLFSBEITSGCOLOKKEIHLYOTFVVOLODPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 INLITHYWYKNSDNDKVQKCSHYLPSBEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA.142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TOMLKLONLVIPWAPENLTIHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEGSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 TOMIKLONIVIPWAPENITLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEGSV 202
                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 INTILITPNGNEDITADFFLITMPTDSLSVSTLPLPEVOCFVFNVRYMCITMNSSSEPQP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and
TILB REFERENCE: REG 2030
CURRENT APPLICATION UNMER: US/09/935.868
CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TOMIKLONIVIPWAPENLTLHKISESQLELNWNNRFINHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                 23 INTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                          61 INLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKRIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                 1 INTTILITINGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LINTTILIPNGNEDTTADEFLTTMPTDSLSVSTLPLPEVOCEVENVEXMNCTWNSSSEPQP
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DYRHKPSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DYRHKFSLPSVDGGKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                ô
       Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1288; DB 9; Length 694; 100.0%; Pred. No. 5.5e-118; tilve 0; Mismatches 0; Indels 0;
                                                                            Indels
Query Match
100.0%; Score 1288; DB 14;
Best Local Similarity 100.0%; Pred. No. 5.4e-118;
Matches 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22. Application US/09935668
Patent No. US20020164690A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.04
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-09-935-868-18
```

us-09-825-561a-4.rapb

```
143 TQMLKLQNLVIPWAPBNLTLHKLSESQLELNWNNRFLMHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1288; DB 14;
Pred. No. 5.5e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 1288;
Best Local Similarity 100.0%; Pred. No. 5.5
Matches 232; Conservative 0; Mismatches
                                                                                                                                                                                                                          S-10-287-035-22
Sequence 22, Application US/10287035
Publication No. US20030104567A1
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-287-035-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-282-162-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                    성 음
                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 INLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNLTLHYWYRNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
TITLE OF INVENTION: AND USING
TITLE OF ILL SPETERAGE: REG 2019A
CURRENT PILLING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USN 09/787,835
PRIOR APPLICATION NUMBER: USN 09/313,942
PRIOR APPLICATION NUMBER: USN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-15
NUMBER OF SEQ ID NOS: 60
SUFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 INTTILIPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYWNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                 INTILITADIGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                     1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1288; DB 14; Length 694; 100.0%; Pred. No. 5.5e-118; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                       Length 694;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                  Query Match
100.0%; Score 1288;
Best Local Similarity 100.0%; Pred. No. 5.5
Matches 232; Conservative 0; Mismatches
             PRIOR APPLICATION NUMBER: PCT/US99/22045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/10287035
Publication No. US20030104567A1
GENERAL INFORMATION:
                            PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 694
TYPE: PRT
CRGANISM: Homo sapiens
US-09-935-868-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100 Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-035-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
```

```
142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOMIKLONIVIPWAPENLILHKISESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING FILE REFERENCE: REG 203DA
CURRENT FILING DATE: 203DA
CURRENT FILING DATE: 2002-11-01
PRIOR PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR PILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR PLICATION NUMBER: 05/313,942
PRIOR PLICATION NUMBER: 06/101,858
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SEQ ID NOS: 60
SEQ ID NO 22
LENGTH: 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LNTTILTPNGNEDITADPFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 INLILLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
TITLE OF INVENTION: AND USING
TITLE OF INVENTION: AND USING
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DYRHKESLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                         203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
```

```
JS-09-824-286-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       챵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 INLILHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 INLILHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 TOMIKLONIVIPWAPENLTLHKLSESQLELNWANRFINHCLEHLVOYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REPERENCE: REG 203-18-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT APPLICATION NUMBER: US/10/282,162
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 3.0
SOFTWARE: FASTSEQ for Windows Version 3.0
SOFTWARE: PRICE CALL OF THE CALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 INTIILTPNGNEDITADFFLITMPTDSLSVSTLPLPEVQCFVFNVEYMNCTMNSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLFEVQCFVFNVBYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMIKLONLVI PWAPENLTLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LINTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOMIKLONIVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 DYRHKFSLPSVDGOKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·
0
                                                                                                                                                                                                                                                                                                                                                                                                           ć
O
                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1288; DB 14; Length 694; Best Local Similarity 100.0%; Pred. No. 5.5e-118; Matches 232; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0;
NUMBER OF SEQ ID NOS: 56
| SOFTWARE FastSEQ for Windows Version 3.0
| SEQ ID NO 18
| LENGTH: 694
| TYPE: PRT
| ORGANISM: HOMO sapiens
| JS-10-282-162-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/10282162 Publication No. US20030143697A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-282-162-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-10-282-162-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ጵ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ዯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ጵ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨ੍ਹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
83 TNLTLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKBIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOWLKLONLVIPWAPENLTLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TNITLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LINTIILIPNGNEDITADFFLITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYRHKFSLPSVDGQKRYMFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 482;
                                                                    APPLICANT: BUXLLY, Linda C
Benjamin, Christopher D
Hession, Catherine A
Histy, Adrian
TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STRESFE: 14 Cambridge Center
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP PC COMPATIBLE
COMPUTER: ISP PC COMPATIBLE
COMPUTER: ISP PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/824,286
FILING DATE: 02-Apr-2001
CLASSIFICATION CAMPATIBLE
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%; Score 1282; DB 9; 99.6%; Pred. No. 1.3e-117; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/017,466
FILING DATE: 10-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A006 PCT CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPRAS: 617 679-2838 INFORMATION FOR SEQ ID NO: 2:
Sequence 2, Application US/09824286
Patent No. US20020028202A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-078-059-3
; Sequence 3, Application US/10078059
                                                                                                                                                                                                                                                                                                               CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.6'
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-286-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
```

```
55 SSEPQPTNLTLHYWYKN-SDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPRROATOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 REHRKOPKOMLKLODLVIPWAPENLTLRNLSEFÖLELSWSNRYLDHCLEHLVOYRSDRDR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNPKFLTPSGNEDIGGKPGTGGDFFLTSTPAGTLDVSTLPLPKVQCFVFNVEYMNCTWNS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWIEGSVDYRHKFSLPSVDGQKRYIFRVRSRFNPLCGSAQHWSEWSHPIHWGSNISKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWIEGSVDHRHSFSLPSVDAQXLYTFRVRSRYNPLCGSAQHWSDWSYPIHWGSNTSKEN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 SSEPQPNNLTLHYGYRNFNGDDKLQECGHYLFSEGITSGCWFGKKEIRLYETFVVQLQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 INTTILIPNGNED-----TTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                               APPLICANT: Ruben et al.
TITE OF INVENTION: CYtokine Receptor Common Gamma Chain Like
FILE REFERENCE: PF466P.
CURRENT APPLICATION: CYTOKINE RECEPTOR COMMON GAMMA CHAIN LIKE
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/269,876
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Moore, Raul A.
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
FILE REFERENCE: PF466F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1999-08-18
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/086,505
EARLIER FILING DATE: 1998-05-22
EARLIER FILING DATE: 1998-05-22
EARLIER FILING DATE: 1998-03-19
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: 09/263,626
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 990.5;
Pred. No. 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/078,563
PRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09376430
Publication No. US20030028006Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.9%;
US20020193305A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 76.2
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFIWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-078-059-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
```

```
133 PKQMLKLQDLVIPWAPENLTLRNLSEFQLELSWSNRYLDHCLEHLVQYRSDRDRSWTEQS 192
                                                                                                                                                                                                                                               61 TNLTLHYWYKN-SDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRQ 119
                                                                                                                                                                                                                                                                                                                      120 ATOMIKLONLVIPWAPENITIHKLSESOLEINWNNRFINHCLEHLVQYRTDWDHSWTEQS 179
                                                                                                                                                                                                          72
                                                                                                                                                                      1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                        16 LNEDI ----GGKPGTGGDFFLTSTPAGTLDVSTLPLPKVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       193 VDHRASFSLPSVDAQKLYTFRVRSRYNPLCGSAQHWSDWSYPIHWGSNTSKEN 245
                                                                                                                                                                                                                                                                                                                                                                                                 180 VDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                   4;
                                                                                               Length 363;
                                                                                                                                 Indels
                                                                                           74.5%; Score 960; DB 10; 76.0%; Pred. No. 4.6e-86; tive 20; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3, 2004, 12:50:51
                                                                                                                                 Conservative
) LENGTH: 363

) TYPE: PRT

; ORGANISM: Homo sapiens

US-09-376-430-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: March
Job time : 31.3268 secs
                                                                                           Query Match
Best Local Similarity
Matches 177; Conserv
                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                 à
```

	RESU 17425 Cips Cips Cips Cips Rita Aiti	A) SC A) SC A) SC A) SC A) NO A) T A) T A) AC A) AC A) AC	A PANA PANA PANA PANA PANA PANA PANA PA
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. M protein - protein search, using sw model tun on: March 3, 2004, 12:31:49; Search time 15.5425 Seconds (without alignments) 1435.834 Million cell updates/sec 1288 Search time 15.5425 Seconds (without alignments) 1435.834 Million cell updates/sec 1 LNTTILTPNGNEDTTADFFLQHWSEWSHPIHWGSNTSKEN 232 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	83366 s its sat ngth: 0 ngth: 2 Minimum Maximum Listing FIR_78:	2: pir2:* 3: pir3:* 4: pir4:* soluts the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES \$ \$ \$ SCORMARIES NO. Score Match Length DB ID	1 1288 100.0 369 2 242565 interleukin-2 rece 2 1097 85.2 373 2 A55718 interleukin-2 rece 4 427.5 33.6 2 14280 common cytckine receptor 5 168.5 13.1 426 2 JC7773 common cytckine receptor 6 159 12.3 389 1 A3255 common cytckine receptor 7 168.5 13.1 426 2 JC7773 common cytckine receptor 8 16.5 11.4 400 2 S06945 gramulocyte-macrop 10 146.5 11.4 400 2 S06945 gramulocyte-macrop 11 135.5 10.5 378 2 S50040 gramulocyte-macrop 11 135.5 10.5 378 2 S50040 gramulocyte-macrop 13 10.2 89.0 1 A33340 gramulocyte-macrop 13 10.2

lactogen receptor interleukin-5 rece interleukin-2 rece granulocyte-macrop glycoprotein 130 - interleukin-6 sign somatotropin recep interleukin-4 rece hematopoietic grow proto-oncogene - m prolactin receptor	REBULT 1 A42555 interleukin-2 receptor gamma chain - human C.Species: Homo sapidna (man) C.Decies: Homo sapidna (man) C.Decies: 104 Mar. 1991 #sequence revision 10-Nov-1994 #text_change 17-Mar-2003 C.Accession: A42555, A46591; Testision 10-Nov-1994 #text_change 17-Mar-2003 C.Accession: A42555, A46591; Testision 10-Nov-1994 #text_change 17-Mar-2003 C.Accession: A42555, A46591; Testision 10-Nov-1994 #text_change 17-Mar-2003 C.Accession: A42555, Mull: 2018	59; 0; Gaps 0; Caps 0; Caps 0; Caps 0; Caps
A34631 A36116 A40267 A40267 A350039 1449699 144699 A50386 S32823 S37622 S37622 S37620	ALIGNM n - human 1.810 18- 32 7 K.; Ish in of the 9233583; 66 with c 00.61h in Of the 9233583; 7 X.; Leo 1. W.; Leo 1. W.; Leo 1. J. C 1.	Score Pred. 0; Mism LITHMPIDS
пипипипипипипипипи	chain chain chail chail chail chail in ID chail in ID chail in ID in	100.0%; 100.0%; ive ; SDTTADFFI
610 610 610 610 610 610 610 610 610 610	gamma e gramma e gramma e gramma e gramma e gramma 256591; H9.2 Ohl 19.2 Oh	100 100 100 100 100 100 100 100
$ \begin{array}{c} \alpha \alpha \alpha \alpha \alpha \alpha \alpha \alpha \alpha \nu \nu$	receptor -1993 #sn -1993 #	Similarity 1 2; Conservati INTTILTPNGNED INTTILTPNGNED INTTILTPNGNED
001 001 001 004 009 009 009 009 009 009 009 009 009	kkin-2 respectively. The control of	Ouery Match Best Local Si Matches 232; 1
₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	RESULT 1 A42565 interleukin-2 C; Date: 04-Ma C; Date: 04-Ma C; Date: 04-Ma C; Date: 04-Ma C; Date: 05-Ma C; Da	Cynery Duery Best I Matche Oy

Biochem. Biophye. Res. Commun. 193, 356-363, 1993 A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of funct A;Reference number: JN0592; MUID:93277575; PMID:8503926 A;Accession: JN0592 A;Accession: JN0592 A;Kesidue: nucleic acid sequence not shown A;Molecule type: mRNA A;Kesidues: 1-36 < KCMM* A;Kesidues: 1-36 < KCMM* A;Kesidues: 1-36 < KCMM* A;Cross-references: DBD:D13565; NID:933684; PIDN:BAA02760.1; PID:9303685 B;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T. Gene 130, 303-304, 1993 A;Title: Cloning and sequencing of the CDNA encoding a mouse IL-2 receptor gamma. A;Reference number: JN0775; MUID:93366191; PMID:8859699	A;Accession: UNO775 A;Accession: WRWS A;Accession: WRWS A;Readdues: 1-369 < xXX A;Readdues: 1-369 < xXX A;Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046 A;Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046 B;Chiu, R.K.; Dougherty, G.J. A;Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain. A;Reference number: 837582 A;Accession: 837582 A;Accession: B7814 A;Residues: 1-350,'8',352-366,'8',368-369 < CHI> A;Residues: 1-350,'8',352-366,'8',368-369 < CHI> A;Residues: 1-350,'8',352-366,'8',368-369 < CHI> A;Residues: 1-350,'8',310,'994 A;Fitle: The murin. A;Reference number: I53398; WID:95104285; PMID:7805729 A;Accession: I53398; WID:95104285; PMID:7805729	A; Status: president and provided from GB/SMB12004.1; PID:GB61555 A; Residues: 1-369 <res.> A; Residues: 1-369 <res.> A; Cross-references: GB:675852; NID:g861554; PIDN:AAB32904.1; PID:g861555 C; Genetics: A; Gene: IL-2Rgamma A; Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3 A; Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3 A; Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3 C; Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta eptors: C; Function: A; Description: receptor for interleukin-2 C; Superfamily: interleukin-2 stimulated growth, and differentiation of T.cells, B.cells, NK c; Superfamily: interleukin-2 receptor gamma chain C; Superfamily: interleukin-2 receptor gamma chain F; 1-22Domain: signal sequence #status predicted <igs #status="" (covalent)="" (igm)="" 1-22domain:="" 11,="" 156;="" 1;="" 1;<="" 23-369="" 2;="" 2e-63;="" 33;="" 369;="" 42;="" 67.2%;="" <igs="" b53.5;="" best="" carbohydrate="" chain="" conservative="" dbb="" ength="" f;="" g6-3%;="" gamma="" gaps="" indels="" interleukin-2="" length="" local="" match="" msanches="" no.="" pred.="" predicted="" product:="" promain:="" query="" receptor="" score="" sequence="" signal="" similarity="" th="" transmembrane=""><th>2 NTTILTPNGNEDTTADFFT 24 SSKVLMSSANEDIKADLII 62 NLTLHYWYKNSDNDKVQK 64 </th></igs></res.></res.>	2 NTTILTPNGNEDTTADFFT 24 SSKVLMSSANEDIKADLII 62 NLTLHYWYKNSDNDKVQK 64
OY 61 TNLTLHYWYKNSDNDKVQKCSHYLPSEEITSGCQLQKKEIHLYQTPVVQLQDPREPRQA 120	RESULT 2 A55718 Interleukin-2 receptor gamma chain precursor - dog C;Species: Canis lupus familiaris (dog) C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999 C;Accession: A55718 R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg, F Genomics 23, 69-74, 1994 A;Title: IL_ZRagamma gene microdeletion demonstrates that canine X-linked severe combined A;Accession: A55718; MUID:95130114; PMID:7829104 A;Accession: A55718 A;Accession: A55718 A;Accession: A55718 A;Accession: A55718 A;Accession: A55718 C;Catter and A;Accession: A55718 A;Catter and A;Accession: A55718	Query Match 85.2%; Score 1097; DB 2; Length 373; Best Local Similarity 82.8%; Pred. No. 6.4e-84; Additional Similarity 82.8%; Pred. No. 6.4e-84; Additional Similarity 82.8%; Addi	RESULT 3 IRBSULT 3 IRBSULT 3 IRBSULT 3 IRBSULT 3 IRBSULT 3 IRESULT 3 IRBSULT 4 ISSULS E mouse mouse) C;Species: Mus musculus (house mouse) C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000 C;Accession: 149280, A47514; JN0592; NN0775; S37582; IS3398 R;Cao, X.; Kozak, C.A.; Liu, Y. R;Cacrence number: A47514; MUD:93391374; PMID:8378320 A;Reference number: A47514; MUD:93391374; PMID:8378320 A;Residues: 1-39 < CACO. A;Residues: Langlared from GB/EMBL/DDBJ A;Recension: A47514 A;Residues: Langlared from GB/EMBL/DDBJ A;Residues: Langlared from GB/EMBL/DDBJ A;Residues: Langlared from GB/EMBL/DDBJ A;Residues: 1-369 < RE2> A;Residues: 1-369 < RE2> A;Residues: 1-369 < RE2> A;Cross-references: GB:L20048; NID:940467; PIDN:AAA39286.1; PID:9404068 B;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.

us-09-825-561a-4.rpr

m

```
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 27-Oct-2003
C;Accession: A39255 #sequence_revision 30-Jun-1993 #text_change 27-Oct-2003
C;Accession: A39255 #sequence_revision 30-Jun-1993 #text_change 27-Oct-2003
R;Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A;Atitles Molecular cloning of a second subunit of the receptor for human granulocyte-mac A;Reference number: A39255; MUID:91088571; PMID:1702217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Cross-references: GDB:126838; OMIM:138981
A, Map posttion: 22q13.1-2q13.1
A, Map posttion: 22q13.1-3q13.1
C;Superfamily: interleukin (II.)-3/IL-5/GM-CSF receptor common beta chain; cytokine receg C;Superfamily: interleukin (II.)-3/IL-5/GM-CSF receptor; duplication; transmembrane protein C;Superfamily: signal sequence #status predicted <&IG>
F;1-16/Domain: signal sequence #status predicted <&IG>
F;17-89/Product: cytokine receptor common beta chain #status predicted <MAT>
F;17-443/Domain: extracellular #status predicted <&IG>
F;250-431/Domain: cytokine receptor homology <CRS1>
F;250-431/Domain: cytokine receptor homology <CRS2>
F;444-460/Domain: transmembrane #status predicted <TMM>
F;441-60/Domain: intracellular #status predicted <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M38275
C;Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prolactin receptor precursor - chicken
C;Species; Gallus Gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C;Accession: JQ1653
R;Tanaax, M; Meda, K; Okubo, T; Nakashima, K.
Biochem: Biophys. Res. Commun. 189, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA A;Reference number: JQ1655; MUID:93075121; PMID:1445292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 LECFFDGAAVLSCSWEVRKE-VASSVSFGLFYKPSPDAGEEECSPVLREGLGSLHTRHHC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLOKKEIHLYQTFVVQLQDPREPRROATOMLKLQNLVIPWAPENLTLHKLSESQLELNWN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 TWKWRY--EHIDHIPEIQYRKDTATWKDSKTE-TLQNAHSMALPALBPSTRYWARVRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 NRFLNHCLEHL-----VQYRTD----WDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 VQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCS----HYLFSEELTSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A;Experimental source: kidney
C;Superfamily: cytokine receptor homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 12.3%; Score 159; DB 1; Length 897; Local Similarity 26.4%; Pred. No. 2.6e-05; Noservative 40; Mismatches 79; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Kerwords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
                                                                                                                                                                                                                                                                                          receptor common beta chain precursor - human
                   ----FNPLCGSAQHWSEWSHPIHWGSNT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRTGYNGI ----- WSEWSEARSWDTES 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA
A, Residues: 1-897 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: JQ1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Gene: GDB: CSF2RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
C;Species: Gallus gallus (chicken)
C;Date: 0.3-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C;Accession: UG7907, H.S.; Fetterer, R.H.
B;Othem. Biophys. Res. Commun. 299, 321-337, 2002
A;Title: Identification of an alternatively spliced isoform of the common cytokine recept R;Reference number: JG7907, MUID:22325486; PMID:12437989
A;Accession: JG7907
A;Molecule type: mRNA
A;Accession: JG7907
A;Molecule type: mRNA
A;Accession: JG7907
C;Accession: JG7907
C;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-426 <-PIE>
A;Residues: 1-426 <-PIE>
A;Cross-references: GB:AY044251
C;Comment: This protein is an functionally binding protein involved in B cell proliferat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQLQKKEIHLYQTFVVQ-----LQDPREPRRQATQMLKLQNLVIPWAPENLTLHKL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 SESQLELNWNNRF-LNHCLEHLVQYRTDWDHSWTEQSVDYRHK---FSLPSVDGQKRYTF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRFEQSEIIQFQAFYVRVNASCNGQTLEIP----SNRMELQNLVKPEAPVNLTIHNM 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 QKKEI---HLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNW 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----FSLPSVDGQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 KNPQNFSSRCLSYEVEVNSTQTDSYNSNSLEVEDKCQNSEFDRNMEGASCFISPGVLXN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 PSPKGVECILFNEEYMICTW-GSGQTILTANYSLYYWYEN--KLPVVECQQYLWDRSVRIG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: JC7773
R;Pierrot, C; Beniguel, L; Begue, A; Khalife, J.
Biochem. Biochem. Bsychession of a functional III-13Ralphal by rat B cells.
A;Title: Expression of a functional III-13Ralphal by rat B cells.
A;Reference number: JC7773; PMID:11573960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 PLPE-VQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.2%; Score 427.5; DB 2;
llarity 42.9%; Pred. No. 3.5e-28;
Conservative 36; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.1%; Score 168.5; DB 2; 25.5%; Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 NN--RFLNHCLEHLVQYRTDWDHSWTEQSVDYRHK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 RVRSRFNPLCGSAQHWSEWSHPIHWGSN-TSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 YVRSKINNYCGNTQLWSEWSVPVFWGNNSTSK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 KRYTFRVRSRFNPLC-GSAQHWSEWSHPIHWG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.54
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-13Ralpha 1 protein - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gene: ch gamma-c-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J;Genetics:
A;Gene: il-13ralphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
```

⋩ 8 ⋩ 9 ⋩ g ጵ 12;

93

86

ጵ 용 ጵ გ à မှ Page

-----KKEIHLYQTFV 107

à 셤 ò 셤 ò В Š 셤

```
A;Cross-references: EMBL:XS4935; NID:g31860; PIDN:CAA38697.1; PID:g31861
R;Raines, M.A.; Lilu, L.; Quan, S.G.; Joe, V.; DiPersio, J.F.; Golde, D.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 8203-8207, 1991
A;Title: Identification and molecular cloning of a soluble human granulocyte-macrophage A;Reference number: A40989; MUID:91376112; PMID:1832774
                                                                                                                                                                                        149 QYFLYIRNSKRRREIRCPYYIQDSGTHVGCHLDNLSGLTSRNYFLVNGTSREIGI--QFF 206
                                                                                                                                                                                                                                                                             108 VQLQDPRE----PRRQATQMLKLQNLVIPWAPENLTLHKLS--ESQLELNWNNRFLNHC 160
                                                                                                                                                                                                                                                                                                                     207 DSLLDTKKIERFNPPSNVTVRCNTTHCLVRW-KQPRTYQKLSYLDFQYQLDVHRKNTQPG 265
                                                                                                                                                                                                                                                                                                                                                                                                                 161 LEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 VQLQDPRE-----PRRQATQMLKLQNLVIPWAPENLTLHKLS--ESQLELNWNNRFLNHC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 DSLLDTKKIERFNPPSNVTVRCNTTHCLVRW-KQPRTYQKLSYLDFQYQLDVHRKNTQPG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 LEHLVOYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---INVSGDLENRYNFPSSEPRAKHSVKIRAADVRIL----NWSSWSE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 TENLL-----INVSGDLENRYNFPSSEPRAKHSVKIRAADVRIL-----NWSSWSE 311
                                                                      -----SCFIYNADIMNCTW-ARGPTAPRDV 148
   5 ILTPN-GNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEXMNCTWNSSSEPQPTNL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S13684; A4089
R;Aahworth, A.; Kraft, A.
Nucleic Acids Res. 18, 7178, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 QYFLYIRNSKRREIRCPYYIQDSGTHVGCHLDNLSGLTSRNYFLVNGTSREIGI--QFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ILTPN-GNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: Cloning of a potentially soluble receptor for human GM-CSF, Reference number: S13684; MUID:91088339; PMID:2148207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     granulocyte-macrophage colony-stimulating factor receptor - human
                                                                                                                                        64 TLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.3%; Score 145.5; DB 2; Best Local Similarity 21.1%; Pred. No. 0.0001; Matches 52; Conservative 43; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 TLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-333 <ASH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-3 receptor beta-subunit - rat
                                                                      109 LLYPNSGREGTAAQNF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: A40989
A,Molecule type: mRNA
Residues: 314-333 <RAI>
A,Cross-references: GB:M73832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AİBFĞSD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 PIHWGSN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|:
266 TENLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 AIBFGS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 PIHWGS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: S13684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
IS6563 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                  셤
                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:118777; OMIM:306250; OMIM:425000
A;Cross-references: GDB:118777; OMIM:306250; OMIM:425000
C;Keywords: GJycoprotein; growth factor receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status predicted <SIG>F;23-440/Product: granulocyte-macrophage colony-stimulating factor receptor #status predicted <FTMM>F;32-3-46/Domain: transmembrane #status predicted <FTMM>F;46,54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent) #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: Expression cloning of a receptor for human granulocyte-macrophage colony-stimul
Reference number: S06944; MUID:90059966; PMID:2555171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA.
Residues: 347-400 <CRO>
Rappold, G.; Willson, T.A.; Henke, A.; Gough, N.M.
sappold, G.; Willson, T.A.; Henke, A.; Gough, N.M.
shomics 14, 455-461, 1992
Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene CSF2
Reference number: A44474; MUID:93052350; PMID:1358805
                                                                                                          (covale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:X17648; NID:g32087; PIDN:CAA35638.1; PID:g32089; Crosser. K.E.; Wong, G.G.; Mathey-Prevot, B.; Nathan, D.G.; Sieff, C.A. roc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991; Title: A functional isoform of the human granulocyte/macrophage colony-stimulating; Reference number: A41286; MUID:91352066; PMID:1715577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tatus: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulocyte-macrophage colony-stimulating factor receptor A precursor - human N;Alternate names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor
F;36-219/Domain: cytokine receptor homology <CRS1>
F;339-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 YFNKNHTSPWTTFNITVTATNEIGSNSSDPQYVDVTSIVQPGSPVNLTLETKRSANIMYL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --NWNNRFL-----NHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRS 203
                                                                                                                                                                                                                                                                                                                                                                            34 IRCRSLEKETFSCWWKPGSDGGLPTNYTL -- FYSKDSEEEIYECPDYR-----TSGPNSC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Homo sapiens (man)
Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 05-Nov-1999
Accession: S06945; A41286; A44474
Gearing, D.P.: King, J.A.; Gough, N.M.; Nicola, N.A.
                                                                                                                                                                                                                                                                                                              38 VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQKCSHYLFSEELTSG---C
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLOKKEIHLYOTEVVOLODPREPRROAT -- OMLKLONLVI PWAPENLTLH-KLSESOLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 'M' 377-400 «RAP»
Cross-references: GB:S48539; NID:g258858; PIDN:AAB23942.1; PID:g258859
Note: sequence extracted from NCBI backbone (NCBIP:117980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.1%; Pred. No. 0.00011;
Matches 52; Conservative 44; Mismatches 90; Indels 61
                                                                                                                                                                     th 11.6%; Score 150; DB 2; Length 831; Similarity 25.0%; Pred. No. 0.00013; 50; Conservative 34; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 RFNPLCGSAQHWSEWSHPIH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 TLDP----GEWSEWSSERH 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: GDB:CSF2RA; CSF2R
                                                                                                                                                                                                   Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA
Residues: 1-400 <GEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S06945
                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                         Query Match
```

10;

Gaps

61;

Indels

Length 333;

63

-----KKEIHLYQTFV 107

Ŋ

Wed Mar

```
the pigeon prolactin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NyAlternate and the strengtor mouse NyAlternate names: IL-4 receptor (Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #text_change 01-Dec-2000 C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 01-Dec-2000 C;Date: 30-Jun-1993 #seckmann, M.B.; March, C.J.; Idzerda, R.L.; Gimpel, S.D.; VandenBos, Widmer, M.B.; Cosman, D.; Park, L.S. (C.J.; Idzerda, R.L.; Gimpel, S.D.; VandenBos, Widmer, M.B.; Cosman, D.; Park, L.S. (A.; Idzerda, R.L.; Gimpel, S.D.; VandenBos, M.Title: The murine interleukin-4 receptor: molecular cloning and characterization A;Reference number: A90911; MUID:90030408; PMID:2805066
        --SCFIYNADLMNCTW-ARGPTAPRDV 148
                                                                                                                                                                                       OYFLYIRNSKRRREIKCPYYIQDSGTHVGCHLDNLSGLTSRNYFLVNGTSRBIGI--QFF 206
                                                                                                                                                                                                                                                                                    VQLQDPRE----PRRQATQMLKLQNLVIPWAPENLTLHKLS--ESQLELNWNNRFLNHC 160
                                                                                                                                                                                                                                                                                                                                                DSLLDTKKIERFNPPSNVTVRCNTTHCLVRW-KQPRTYQKLSYLDFQYQLDVHKKYTQPG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQXRYTFRVRSRFNPLCGSAQHWSEWSH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 KNHTNPWTTYNITVMAMNEIGSNSSDPQYVDVTSIVQPDAPVNLSLETKTSASTTYLLAK 149
                                                                                                                           64 TLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQ------KKBIHLYQTFV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 KKEIHLYOTFVVOLODPREPRROAT -- OMLKLONLVIPWAPENLTLH----KLSESOLELN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCDLQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 IRCRSLEKETESCWWKPGSDGGLPTNYTL--FYSKDSEEKIYECPDYGMSG--PNSCYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382;Superfamily: cytokine receptor homology <CRS1>;20/Domain: cytokine receptor homology <CRS1>;240-426/Domain: cytokine receptor homology <CRS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 WANTEL-----NHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinology 135, 269-276, 1994
A)Title: Cloning, expression, and mutational analysis of A)Ritle: Cloning, expression, and mutational analysis of A)Recession: 150455, MUID:94283267; PMID:7516866
A)Recession: 150455
A)Ratus: preliminary; translated from GB/EMBL/DDBJ
A)Rolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quefy Match 10.3%; Score 132.5; DB 2; Best Local Similarity 22.2%; Pred. No. 0.0037; Matches 44; Conservative 37; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interleukin-4 receptor precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----IGEWSEWSSERH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 NPLCGSAQHWSEWSHPIH 223
109 LLYPNSGREGTAAONF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: I50455
Chen, X.; Horseman, N.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 AİBF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 PIHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .. 'n
                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                        108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                        ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                               C'Accession: I56563 ... Sauter, A.; Gebicke-Haerter, P.J. J. A.; Sauter, A.; Gebicke-Haerter, P.J. J. Sauter, B.J. J. Sauter, A.; Gebicke-Haerter, P.J. J. Sauter, B.J. Sauter, J.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: interleukin (IL)-3/IL-5/GW-CSF receptor common beta chain; cytokine recep; Keywords: cytokine receptor ;39-235/Domain: cytokine receptor homology <CRS1>;253-433/Domain: cytokine receptor homology <CRS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: alternative splicing; glycoprotein; growth factor receptor; transmembrane pd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Species: Alone sapiens (man)
C;Date: 20. Feb-1995 #text_change 05-Nov-1999
C;Accession: S50040; S47568
R;Hu, X.; Zuckerman, K.S.
submitted to the EMBL Data Library, March 1994
A;Description: Cloning and sequencing of the cDNA encoding alternative splicing variants
A;Reference number: S50039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-78 eHTN.
A; Cross-references: EMBL:129349; NID:g460284; PIDN:AAA60962.1; PID:g463107
A; Cross-references: EMBL:1229349; NID:g460284; PIDN:AAA60962.1; PID:g463107
B; Hu, X.; Emanuel, P.D.; Zuckerman, K.S.
Biochim: Biochims Brockyye, Acte 1223, 306-308, 1994
Biochim: Biochyye, Acte 1223, 306-308, 1994
A; Title: Cloning and sequencing of the cDNAs encoding two alternative splicing-derived
A; Reference number: S47567; MUID:94368898; PMID:8086503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ranulocyte-macrophage colony-stimulating factor receptor alpha-3 chain - human
Alternate names: GM-CSF receptor alpha-3 chain, hematopoietic growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 LOCFFDGIOSLNCSWEVWTK-VTDSVSFGLFYSSSPKAGEKKCSPVV--KELQASRYTRY 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCSINVSDPAAHSQYTVSVK----RLEQGKFIESFN-HIQMNPPTLNLTKNRDS-YSLH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINNR-----FLINHCLEHLVQYRTD---WDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ILTPN-GNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNL 63
                                      #sequence_revision 26-Jul-1996 #text_change 27-Oct-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYRNSDNDKVQKCSHYLFSEELTSG----
                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-896 <RES>
A;Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.6%; Score 136.5; DB 2;
Best Local Similarity 23.9%; Pred. No. 0.0019;
Matches 48; Conservative 41; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5%; Score 135.5; DB 2
20.5%; Pred. No. 0.00081;
tive 43; Mismatches 90
                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTIPEYKGL - - WSEWSNECTW 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFNPLCGSAQHWSEWSHPIHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 241-315,317-378 <HUW>
A,Cross-references: EMBL:129349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 20.5%
Matches 50; Conservative
Species: Rattus sp. (rat)
Date: 26-Jul-1996 #sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: GM-CSF-RA3; CSF3RA
                                                                                                                                                                                                                                                                            A;Accession: I56563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S47568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rIL-3Rbeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418
```

ઠે В à g ò В à Ы 7;

8

ŏ

11;

97

296

144

```
A,Cross-references: GB:M34397, NID:g191821, PIDN:AAA37204.1, PID:g309101
A,Cross-references: GB:M34397, NID:g191821, PIDN:AAA37204.1, PID:g309101
C;Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor C;Superfamily: interleukin (IL)-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor; duplication; transmembrane protein
C;Keywords: cytokine receptor; duplication; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-3-96/Forduct: cytokine receptor common beta chain #status predicted <MAT>
F;3-441/Domain: extracellular #status predicted <cal>
F;39-235/Domain: cytokine receptor homology <CRST>
F;39-235/Domain: cytokine receptor homology <CRST>
F;39-235/Domain: cytokine receptor homology <CRST>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPDYK-----TGGPNSCYFSKGHTSIWKOKYVITVNAINQMGISSSDPLYVHVTYIVEPEP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 QATQMLKLQN-----LVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYR--- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 KEPPGASVYTRYHCSLPVP-EPSAHSQYTVSVKHLEQGKFIMSYNHIQMEPPTLNLTKNR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESQLELNWNNR-----FLNHCLEHLVQYR---TDWDHSWTEQSVDYRHKFSLPSVDGQKR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FIIQYEIRL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                projectin receptor - bovine (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: 145911
C;Accession: 145911
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol: 89, 47-58, 1992
A;Title: Molecular cloning of the bovine projactin receptor and distribution can appear to the project of the bovine project of the position of A;Reference number: 145971
A;Accession: 145971
A;Reference rumber: 145971
A;Reference number: 15871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 DS-YSLAMETQKMAYSFIEHTFQ--VQYKKKSDSWEDSKTE-NLDRAHSMDLSQLEPDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 VQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSVSTL---PLPE----VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSVSLINGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGLPTNYTLTY-HKEGET-LIHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
9.7%; Score 125; DB 1; Length 896;
Best Local Similarity 23.1%; Pred. No. 0.017;
Matches 48; Conservative 36; Mismatches 82; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PANLTLELKHPEDRKPYLWIKWSPPTMT-----DVKSGW
                                                                                                                                                                                                                                                                                                                                                                                                      F;253-434/Domain: cytokine receptor homology <CRS2>
F;442-463/Domain: transmembrane #status predicted <TWM>
F;464-896/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSHYLFSEEITSG----CQLQKKEIHLYQTFVVQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 KE---IHLYQTFVVQLQDPREPRRQATQMLKLQNLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.4%; Score 121.5; DE
25.4%; Pred. No. 0.02;
.ve 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: PRLR
C,Superfamily: cytokine receptor homology
F,36-221/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 YTFRVRSRFNPLCGSAQHWSEWSHPIHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCARVRVK--PISNYDGIWSKWSEEYTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 25.4%; ses 60; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rigorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K. Proc. Natl. Acad. Sci. U.S.A. 87, 5453, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A,Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein A,Reference number: A33582; MUID:9031931; PMID:1695379
                                                                                                                                        A Molecule type: mRNA
A; Residues: 1-258 < w02>
A; Residues: 1-258 < w02>
A; Residues: 1-258 < w02>
A; Residues: 1-254; PSMENL' < w03>
A; Residues: 1-254; PSMENL' < w03>
A; Residues: 1-254; PSMENL' < w03>
A; Residues: 1-254; PSMENL' < w03>
A; Residues: 1-254; PSMENL' < w03>
A; Note: part of this sequence, including the amino end of the mature protein, was confir A; Note: part of this sequence, including the amino end of the mature protein, was confir A; Note: part of this sequence, including the amino end of the mature protein, was confir accelulat domain and may encode a soluble form of the receptor R; Harada, N.; Castle, B.E.; Gorman, D.M.; Iroh, N.; Schreurs, J.; Barrett, R.L.; Howard, Proc. Natl. Acad. Sci. US.A. 87, 857, 861, 1990
A; Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor based of A; Reference number: A34861; MUID:90138976; PMID:2405398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression and poten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:34-219/Domain: cytokine receptor homology <CRS>
F:234-257/Domain: transmembrane #stetus predicted <TMM>
F:228-810/Domain: intracellular #status predicted <INT>
F:72.129,135,163,177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPSGNVKPLAPDNLTLHTNVSDEWLLTWNNLYPSNNLLYKDLISMVNISREDNPAEFIVY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNDKVQKCSHYLFSEEIT-----SGCQLQKKEIHLYQTFVVQLQDPREPRRQATQML 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RIMFFEFSENLTCIPRNSASTVCVCHMEMNRPVQSDRYQMELWAEHROLWQGSF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 KLONLVIPWAPENLTLHKLSESOLELNWNNRFLNHCL--EHLVQY----RTDWDHSWTEQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 TTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTW-NSSSEPQPTNLTLHYWYKNS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine receptor common beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 27-Oct-2003
C;Accession: A35782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      †SVGCLILLLVTGSGSIKVLGEP--TCFSDYIRTSTCEWFLDSAVDCSSQLCLHY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:M29854; NID:g198346; PIDN:AAA39297.1; PID:g309407 Wrighton, N.C.; Campbell, L.A.; Lee, F.D. rowth Factors 6, 103-118, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      saidues: 1-73, T',75-333, P',335-810 <RES>
ross-references: GB:M64879; NID:g198359; PIDN:AAB59727.1; PID:g198361
                                                                        Cross-references: GB:M27959; NID:g198363; PIDN:AAA39299.1; PID:g309408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title: The murine interleukin-4 receptor gene: Genomic structure, Reference number: 154232; MUID:92265335; PMID:1534014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVDY----RHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 NVTYKEPRLSFPINILMSGVYYTARVRVRSQILTGT---WSEWSPSITW 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Introns: 24/1, 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2; Superfamily: interleukin-4 receptor; cytokine receptor homology; Reywords: alternative splicing; cytokine receptor; glycoprotein, 1-25/Domain: signal sequence #status predicted <21G>, 256-810/Product: interleukin-4 receptor #status experimental <WAT>, 26-233/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 132; DB 1; Length 810; 26.2%; Pred. No. 0.004; tive 28; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 60; Conserv
Molecule type: mRNA
Residues: 1-810 <MOl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA;Residues: 1-810 < HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: I54232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A34861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
```

ð

심 ò 셤

셤 ð

à

of prolact:

17;

Wed Mar 3 15:49:09 2004

us-09-825-561a-4.rpr

173 KPEKATDWETHFTLKQTQLK-IFNL--YPGQK---XLVQIRCKPDHG---YWSEWS 219

Search completed: March 3, 2004, 12:38:59 Job time : 16.5425 secs

qq

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	Run on: March 3, 2004, 12:31:14; Search time 37.9085 Seconds (without alignments) 1930.971 Million cell updates/sec	Title: US-09-825-561A-4 Perfect score: 1288 Sequence: 1 LNTILTPNGNEDTTADFFLQHWSEWSHPIHWGSNTSKEN 232	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 1017041 segs, 315518202 residues	Total number of hits satisfying chosen parameters: 1017041	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : SPTREMBL_25:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_invartebrate:* 6: sp_mammal:* 7: sp_mc:* 8: sp_prammal:* 10: sp_phage:* 11: sp_vartebrate:* 12: sp_virus:* 13: sp_virus:* 14: sp_unclassified:* 15: sp_virus:* 16: sp_bacteriap:* 17: sp_archeap:*
--	---	---	---	--	--	--	---	---	--

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q8sq71 sus scrofa	Osvhr8 rattus norv	Q7tp53 rattus norv	Osaup2 gallus gall	Osavo7 gallus gall	Ogdedl oncorhynchu		O90xp8 oncorhynchu	0951f0 canis famil	Q8vhk6 rattus norv	O88786 mus musculu	Osbran4 mus musculu	Q8c1z3 mus musculu	Q7tt27 mus musculu	Q96bb4 homo sapien	Olyrv5 macaca fasc
SUMMARIES	QI	088071	Q8VHR8	Q7TP53	QBAUP2	Q8AV07	Q9DEQ1	Q8JJD1	Q90XP8	Q95LP0	Овинке	088786	Q8BNM4	Q8C1Z3	Q7TT27	Q96BB4	Q7YRV5
	DB	9	11	11	13	13	13	13	13	v	11	11	11	11	77	4	9
	Query Match Length DB	368	278	448	348	374	343	313	404	386	385	383	424	424	442	427	409
de	Query	77.4	71.4	51.8	33.2	33.2	22.0	21.7	20.1	16.5	15.9	15.5	14.2	14.1	14.1	13.8	13.7
	Score	997.5	919	667.5	427.5	427.5	283.5	279.5	259.5	213	204.5	199.5	183.5	181.5	181.5	178	177
	Result No.	н	7	ო	4	ហ	9	7	80	Q	10	11	12	13	14	15	16

Q951f1 canis famil Q8vhc2 rattus norv	Q9nc/s nome Bapien Q863z6 Bus scrofa O7t2z0 gallus gall	Q8wx09 homo sapien	Ogudy5 homo sapien	Oyzlao cavia porce	057519 xenoous lae	097597 bos taurus	Q64146 rattus norv	Q9h5r3 homo sapien	Q8qzx9 mus musculu	Q8cbw5 mus musculu				-				Q9wtm8 rattus norv	Q63257 rattus norv	Secile musculu	Q9jiq7 mus musculu	O9jmd5 musculu	ednna	mus
																	5.5			54	7 -			
Ŋ					. o		ý		6	ī	و	0	0	м	9	9	00		7	0	7	'n	٠,	œ
Q95LF1 Q8VHC	Q863Z6 O7T2ZG	Q8WX09	Q9UDY5	0921A0	05751	097597	06414	Q9H5R3	O80ZX	OBCBW	Q9IBP	Q9PT10	05469	Q60583	D9PTH	COMED9	Q9R1WB	MILM 60	06325	QBCII	Q9J1Q7	OMP 60	QBMIR9	оэллна
117	9 4	4	4;	= =	12	G	11	4	Ξ	11	13	13	11	H	13	13	류	1	11	11	ij	11	9	11
4 0 5 4 2 6	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	249	279	204 201 Оп	881	349	896	232	896	810	611	611	810	810	611	918	229	801	800	359	370	359	803	359
13.4	12.0	11.0	11.0	10.8	10.7	10.6	10.6	10.6	10.3	10.2	10.1	10.1	10.1	o.	7.6	7.6	4.	9.4	о .3	9.2	9.	9.1	9.1	9.0
172.5	154.5	141.5	141.5	7.7.F	137.5	137	136.5	136	132.5	132	130	130	130	128	125	124.5	120.5	120.5	119.5	118.5	118.5	117.5	117.5	116.5
17	- 12ਰ	22	53	# LC	9	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	7	1 3	44	5
	1 (1) (1)	• • •	•••	•••	• • •							٠.							•		•	•	•	•

ALIGNMENTS

.	਼, ਜ ਼ਾ
	Gaps
Euteleostomi, Sus Sus r gamma.", ases	ं हैं 8 90 90
e) Enteleos Sus Sus Sus Cor gamma.' ibases (D200-doma)	C64, Length 368 Indels
nate) pdate) pdate) nuidae; datab	ADFD7 CRC DB 6; L e-86; 1
11 10 10 10 10 10 10 10 10 10 10 10 10 1	741 741 741 741
PRT; 368 AA. Created) Last sequence up Last amnotation; Craniata, Vert dactyla; Suina; EMBL/GenBank/DDB. IEA. tin/interferon-c. ctivity; IEA.	Fami, PF00041; fh3; 1. PROART; SM00060; FM3; 1. RECEPTOR: 368 AA; 41810 WW. 43643AB0741 SEQUENCE 368 AA; 41810 WW. 43643AB0741 FY Match 77.4%; Score 997 5; L Local Similarity 78.9%; Pred: No. 4.5 ches 183; Conservative 18; Mismatches
MBLrel. 21, Created) MBLrel. 21, Last sequebler 21, Last sequebtor gamma. ceptor gamma. ca; Chordata; Craniat ia; Cetartiodactyla; A. A. A. R. R. R. R. R. R. R.	MY: 43 SOOI Pred
RY; 11. 21, 12. 21, 12. 23, 12. 25, 12. 25, 12. 25, 12. 25, 12. 25, 12. 25, 13. 25, 14. 25, 15. 11. 25, 17. 11. 11. 11. 11.	1. ATOPO 1810 M 77.4%; 77.4%; ive
1 1 108071 PRELIMINARY, 080071 01-JUN-2002 (TERMELRel. 21, 01-JUN-2002 (TERMELRel. 21, 01-JUN-2002 (TERMELRel. 21, 01-JUN-2002 (TERMELRel. 25, 01-JUN-2002 (TERMELRel. 25, 01-JUN-2002 (TERMELRel. 25, 01-JUN-2002 (TERMELRel. 25, 01-JUN-2002 (TERMELRel. 21, 01-JUN-2002 (TERMELRel. 21, 01-JUN-2002 (TERMELRel. 25, 01-JUN-2002 (TERMELRel. 25, 02-JUN-2002 (TERMELRel. 25, 03-JUN-2002 (TERMELRel. 25, 03-JUN-2002 (TERMELREL) (TERMELREL) 03-JUN-2002 (TERMELREL) (TERMELREL) 03-JUN-2003 (TERMELREL) (TERMELREL) 03-JUN-2003 (TERMELREL) (TERMELREL) 03-JUN-2003 (TERMELREL) (TERMELREL) 03-JUN-2003 (TERMELREL) (TERMEL	Pfami PF00041; fn3; 1: SMART; SM00060; FN3; 1: PROSITE; PS01355; HEMATO) RECEPTOR: 368 AA; 4181 SEQUENCE 368 AA; 4181 L Local Similarity 78: Ches 183; Conservative
PRELIMIN 12 (TrEMBLA 13 (TrEMBLA 13 (TrEMBLA 13 (TrEMBLA 13 (TrEMBLA 14 (Fig) 16 (Fig) 17 (Fig) 18 (Fig) 1	041; ffi3; 0060; FN3 501355; H 368 AA; 368 AA; milarity Conserv
1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Pfam; PF00041; fm3) PMART; SM00060; FM3 PROSITE; PS01355; H Receptor. SEQUENCE 368 AA; CY MATCh L Local Similarity Chee 183; Conserv
ULT 1 088071 088071 01-JUN- 01	Proposition Processing States of Sta
28.2011 10.2020 20.	######################################

al Simitaticy
183; Conservative 18; Mismatches 30; indeis
1 LATTILIPHONEDITADFELTMPTDSLSVSTLPIDEVOCEVENVEYMNCTMNSSSEPOP 60

ò

PRT;

PRELIMINARY;

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8AUP2
   SORTARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRAINSDEAGUE ACCOUNT.

CASALTA MAIGHT.

                                                                                                                                                                                                180
                                                                                                                                                                                                                                                         143 PQTLKLODLVIPWAPANLTLRTLSESQLELNWSNRYLDHCLEHLVQYRSDRDRSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 NLTWHYRYKGSDNWTFQECSHYLFSKEITSGCQIQKEDIQLYQTFVVQLQDPQKPQRRAE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 OKINIONIVIPWAPENLTLYNLSESOVELRWKSRYIERCLOYLVOYRSNRDRSWTEGIVD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
INPKVLTHSGNEDITADFLLLSTPPGTLNVSTLPLPKVQCFVFNVEYMNCTWNSSSELQP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SSKVIAMSSGNEDIKSDLLLISMDLKHISVPTLPLPEVQCFVFNVEYMNCTWNSSSEPQPT
                                                                  TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDFREPRRQA
                                                                                                     OMLKLONLVI PWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                  |:|
DHRQSFSLPSVDAQKLYTFRVRSRYNPLCGSAQRWSDWSHPIHWG-NTSKEN 253
                                                                                                                                                                                                                                                                                                                           DYRHKPSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 YRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
71.4%; Score 919; DB 11; Length 2
Best Local Similarity 70.6%; Pred. No. 8.6e-79;
Matches 163; Conservative 33; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
278 278 278 MW; 4011F8F774804CDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequenc)
01-OCT-2003 (TrEMBLrel. 25, Last annotate)
Cytokine receptor gamma chain (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxiD=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
NON TER
NON TER
SEQUENCE
                                                                                                                          83
                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VHR8
                                                               ઠે
                                                                                                                       g
                                                                                                                                                                                             à
                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ਨੇ
```

RESULT Q7TP53

```
66 HYW-YKNSDNDKVQKCSHYLFSEEIISGCQLQKKEIHLYQTFVVQLQDPREPRRQATQML 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 KLONLVIPWAPENLTLHKLSESQLELNWNNRFINHCLEHLVQYRTDWDHSWTEQSVDYRH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 HDWRYKGSDINNTFQECSHYLFSKEITSGCQIQKGEDIQLYQTFVVQLQDPQKPQRRAEQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=white leghorn SC, and Leghorn; TISSUE=Liver, and Spleen;

MEDLINE=22325466; PubMed=12437989;

Min W. Lillehof HS., Fetterer R.H.;

I'dentification of an alternatively spliced isoform of the common cryckine receptor gamma, Greek chain in chickens.";

Elochem. Biophys. Res. Commun. 299:321-327(2002).

EMBL; AJ41989; CAD12042.1; -..

REMEL; AJ41989; CAD12043.1; -..

REMEL; AJ41989; CAD12043.1; -..

REMEL; AJ41989; CAD12043.1; -..

RO; GO:0016020; C:membrane; IEA.

RO; GO:0016020; C:membrane; IEA.

RO; GO:0016020; C:membrane; IEA.

RO; GO:0016020; C:membrane; IEA.

InterPro; IPR003996; KR.H.

InterPro; IPR003961; FN.III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MR-2003 (TrEMBLrel. 25, Last sequence update)
Putative common cytokine receptor gamma chain a precursor.
Gallus gallus (Chicken).
Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Archosauria, Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                    Agarus Auzyszykusa (Agal)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                 Xu C.S., Ii W.Q., Li Y.C., Wang L., Wang S.F., Han H.P., Wang G.J. Chai L.D., Yuan J.Y., Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
"Liver regeneration after PH.";
Submitted (JUN -2003) to the BMBL/GenBank/DDBJ databases.
BMBL; AY325195; AAP92596.1;
BRBL; AX325195; AAP92596.1;
SEQUENCE 448 AA; 51863 MW; EBDS6D1FA86614D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 RFSLPSVDEOKLYTFRVRSRFNPICGSTQQWSKWSQPIHWGSHTAEEN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 KFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 21 POTENTIAL
348 AA; 39750 MW; 93DEC9F15DE9BBE6 CRC64;
(TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003531; Hemtopoptn_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.2%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Signal.
                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
01-OCT-2003 (
01-OCT-2003 (
01-OCT-2003 (
```

ઠે 셤 셤

ઠે

g හි g

ઠે

```
80 SYDKSDRFRILKTKLV---HQNMSYVQDHNIKSMYKLYPPVNLSVEMNKDPELNLYMNNS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 KNTFCIESEVRYRINSD-KWKTSTPSKEQKYAVAFPLKSSRYBFQVRARVNDMCGESEFW 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 FLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHW 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 PNVNCLIINLDYVNCIWSEQSIPE-VNFT--FFSSRFIKDNMEECTTYLQEESYAVGCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 OKKEIHLYQTFVVQLQDPREPRRQATGMLKLQNLVIPWAPENLTLHKLSESQLELNWNNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 PEVOCEVENVEYMNCTWNSSSEPOPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITRE-21887902; PubMed=11394690;
Wang T., Secombes C.J.;
"Cloning and expression of a putative common cytokine receptor gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
Fish and Shellfish Immunol. 11:233-244(2001).
EMBL, AJ276623, CAC09429.2;
InterPro; IPR003961; F:receptor activity; IEA.
SMATT: SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Soma G., Inagawa H., Honda T., Nishizawa T., Kanou J., Endo M.,
Otochake M., Nakanishi T.;
Rainbow trout cytokine receptor common gamma chain precursor (IL-2R
gamma chain) like protein.";
                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-DRC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytokine receptor common gamma chain.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota, Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 22.0%; Score 283.5; DB 13; Length 343; Local Similarity 30.9%; Pred: No. 1.4e-18; Conservative 37; Mismatches 88; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 AA; 39486 MW; ED8429E7534B21EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation Update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine receptor common gamma chain precursor IL2RGAMMA.
                             190 YVRSKINNYCGNIQLWSEWSVPVFWGNNSISK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 AA.
                                                                                                                                                               343 AA.
  200 RVRSRFNPLCGSAQHWSEWSHPIHWGSN-TSK
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 SEWSHPIHWGS 226
                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 SEWSOPIOWOS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08JJD1
08JJD1;
                                                                                                                                                               Q9DEQ1
                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               吕
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
    Š
                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22325486; PubMed=12437989; Min W. Lillahoj H.S., Fetterer R.H.; Min W. Lillahoj H.S., Fetterer R.H.; Cattorion of an alternatively spliced isoform of the common cytokine receptor gamma, Greek chain in chickens."; Elochem. Biophys. Res. Commun. 299:321-327(2002). Bib.; AJ418896; CAD12041.1; E.A. GO; GO:0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:004872; F:receptor activity; IEA. InterPro; IPR002966; F:hematopoietin/interferon-class (D200-domain. ..; IEA. RO; GO:004872; F:receptor activity; IEA. InterPro; IPR003961; FN III.

InterPro; IPR003561; FN III.

InterPro; IPR003561; FN III.

Rem: PF00041; fin3; 1.

Rem: PF00041; fin3; 1.
                                                                       <u>ئ</u>
                                                                                                                                                                                                                                      CQLOKKEIHLYQTFVVQ------LQDPREPRRQATQMLKLQNLVIPWAPENLTLHKL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGNOLOLIWSSPYPKEQCLEHVVKYKSNKDISWINOEV----KGVIFSFPSVDYEKYYIF 189
                                                                                                                                                                                                           COLOKKEIHLYQTFVVO-----LQDPREPRQATQMLKLQNLVIPWAPENLTLHKL 143
                                                                                                                                                                                                                                                                                                                                               SGNÓLOLTWSSPYPKEOCLEHVVKYKSNKDTSWTNOEV----KGVIPSPPSVDYBKYYTP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SESQLELNWNNRF-LNHCLEHLVQYRTDWDHSWTEQSVDYRHK---PSLPSVDGQKRYTF 199
                                                                                                                34 PLPE-VOCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSBEITSG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                              24 PSPKGVECILENEENMICTW-GSGQTLTANYSLYYWYEN--KLPVVECQQYLWDRSVRIG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 PSPKGVECILFNEEYMTCTW-GSGQTLTANYSLYYWYEN--KLPVVECQQYLWDRSVRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 PLPE-VOCFVFNVEYMNCTWNSSSEPQPINLTLHYWYKNSDNDKVQKCSHYLFSEEITSG
                                                                                                                                                                                                                                                                                                   SESQLELNWNNRF-LNHCLEHLVQYRTDWDHSWTEQSVDYRHK---FSLPSVDGQKRYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative common cytokine receptor gamma chain b precursor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                       Gaps
                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.2%; Score 427.5; DB 13; Length 374; 42.9%; Pred. No. 3.7e-32; tive 36; Mismatches 56; Indels 29;
                        DB 13; Length 348;
                                                                       56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL 1 21 POTENTIAL.
SEQUENCE 374 AA; 42547 MW; B3A62E0D4D02B42B CRC64;
                      33.2%; Score 427.5; DB 1.
42.9%; Pred. No. 3.4e-32;
tive 36; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                              200 RVRSRFNPLCGSAQHWSEWSHPIHWGSN-TSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                         190 YVRSKINNYCGNTQLWSEWSVPVFWGNNSTSK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
Query Match
Best Local Similarity 42....
Best Local Similarity 62....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 42.9%
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                   144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBAV07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8AV07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
```

ઠે 윱

g ઠે

셤

ઠે

155

95 79

Gaps

7 ;

```
321 RGFWSDWS---HWSCHSDTES 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
Wu A., Low W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8VHK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
Q8VHK6
                                                                                                               Q95LF0
                                                                                                                                                음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAT THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF THE BOOK OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 ERIPRHCLEYEVEAREEGVGGQPLLQRNVTNEMTLTSLSMDGARRKCFRVRSRMHYCAD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SO SYDKSDRERTLKTKLV---HQNMSYVQDHNLKSMVKLYPPVNLSVEMNKDPELNLYWNNS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIHLYOTF---VVOLODPREPRROATOMIKLONLVIPWAPENLTLHKLSESQLELNW----N 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 NRFLNHCLEHLVQYRTD -- WDHSWTEQSVDYRHKFSLPSVDGOKRYTFRVRSRFNPLCGS 211
                                                                                                                                                                                                                                                                                                                                                                                                                             96 OKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNR 155
                                                                                                                                                                                                                                                                                                                ტ
ს
                                                                                                                                                                                                                                                                                                                                                  23 PNVNCLIINLDYVNCIWSEQSIPE-VNFT--FFSSRFIKDNMSECTTYLQEDSYAVGCRL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 CFVFNVEYMNCTWNSS-SEPQPTNLTLHYWYXNSDNDKVQKCSHYLFSEEITSGCQLQKK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diockyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J., Secombes C.J.; Jones C.S., Noble L.R., Verspoor E., Holland J., Secombes C.J.; and characterization of a putative mykiss) "; alpha-2 sequence from rainbow trout (Oncorhynchus mykiss) "; submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AFS61437; AALS6927.1; -.
GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR002996; CRIA.

InterPro; IPR0089957; FU_III-like.
                                                                                                                                                                                                                                                                                                                36 PEVQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 FLNHCLEHLVOYRTDWDHSWTEQSVDYRHKFSLPSVDGOKRYTFRVRSRFNPLCGSAQHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.1%; Score 259.5; DB 13; Length 404; 27.9%; Pred. No. 3.1e-16; ative 44; Mismatches 88; Indels 13; Gaps
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amotation update)
01-OCT-2003 (TrEMBLrel. 25, Last amotation update)
11terleukin 13 receptor alpha-2.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metacoa, Chordata, Cramiata, Verfebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Protacanthopterygiis Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                              Query Match 21.7%; Score 279.5; DB 13; Length 313; Best Local Similarity 30.4%; Pred. No. 2.9e-18; Matches 58; Conservative 38; Mismatches 88; Indels 7;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB042024; BAB91242.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                  SIGNAL 1 14 POTENTIAL.
SEQUENCE 313 AA; 36259 MW; 28278777AF2F9BF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 AA; 46728 MW; 4B9B7E3F4CFFB6D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AOHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 SEWSHPIHWGS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 SEWSQPIQWDS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                     Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90XPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
         TKU KE S
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
```

```
125 TTYWTSPOGNRET------KIQDMDCVYYNWQYLVCSWKPGMGVHFD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 QATQMIKLQNLVIPWAPENLTLHKLSESQLELNWN---NRFLNHCLEHLVQYRTDWDHSW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 PSYFIFQLQNIVKPWPPDYLSLTVKNSEEINLKWNMPKGPIPAKCFIYEIEFTED-GTTW 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TILLI-PNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMVCTWNSSSEPQ-P 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Libsuca. Immunojathol. 79:181-195(2001).

EMBL; AF314533; AAL14887.1; -

EMBL; AF314533; AAL14887.1; -

EMBL; AF314533; AAL14887.1; -

EMBL; AF314533; AAL14887.1; -

GO; GO:0016896; F:nematopolaterin/interferon-class (D200-domain. . .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR002996; CRIA.

InterPro; IPR003995; FW IIII-like.

InterPro; IPR003932; Hemitopolate. S. F2.

PROSITE; PS01356; HEMATOPO_REC_$\overline{S}_F2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 INLILHYWYKNSDNDKVQKCSHYLPSEEITSGCQLQKKEIHLYQTFVVQLQDPRE--PRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 TEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 VITIVENEIQITRISNESQK-LCFLVRSKVNIYCSDDGIWSEWSDEQCWKGDIWKE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of canine IL-13 receptor alpha chain (alphal and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues.";
                                                                                                                                                                                                          Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 16.5%; Score 213; DB 6; Length 386; Local Similarity 25.8%; Pred. No. 7.3e-12; Les 61; Conservative 38; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE 386 AA; 45110 MW; A16FDF2DD023ED95 CRC64;
                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Interleukin 13 receptor alpha chain 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2002 (TrEMBLrel. 20, Created)
1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Interleukin 13 receptor alpha chain 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 385 AA.
386 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21287533; PubMed=11389954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
PRELIMINARY;
```

S

ਨੇ 셤 ò

g

ਨੇ

```
44482 MW; C25212325C47E35B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 FRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVRCKVNIYCADDGIWSEWSEEECWEGYTGPDS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%; Score 183.5; DB 28.1%; Pred. No. 5e-09; tive 37; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 TFRVRSRFNPLC-GSAQHWSEWS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.1%;
Matches 57; Conservative
                                                                       Query Match
Best Local Similarity 25.7%
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin 13 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                          383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBBNM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8BNM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28BNM4
                                                                                                                                                                          ò
                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 TLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQL--QDPREPRQAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 OMLKLONLVIPWAPENLTLHKLSESOLELNWN---NRFLNHCLEHLVOYRTDWDHSWTEQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 MVFQLQNIVKPLPPEFLHISVENSIDIRAKWSTPGGPIPPSCYTYEIVVRED-DISW-ES 281
                  expression in rat tissues."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR448818; AAL57313.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
GO; GO:0004895; F:receptor activity; IEA.
InterPro; IPR003996; FN III-like.
InterPro; IPR008957; FN III-like.
InterPro; IPR008957; FN III-like.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
"Molecular cloning of rat interleukin 13 receptor alpha 2 gene and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins M.; "The murine IL-13 receptor alpha 2: molecular cloning, characterization, and comparison with murine IL-13 receptor alpha 1."; J. Immunol. 161:2317-2324(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 NGNED----TTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWN-SSSEPQPTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C3H/HEJ; TISSUE=Thymus;
MED/LINE=98391042; PubMed=9725226;
Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 ATDKNDMKLKRRANESEDLCFFVRCKINIYCADDGIWSEWSEECWEGYTGPDS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 SVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; UG5747; AAC33240.1;
R EMBL; BC003723; AAH03723.1;
R HSSP; P16471; 1BP3.
R GO; MG1:1277954; Ill3raz.
R GO; GO:0004896; F:membrane; IRA.
GO; GO:0004896; F:membrane; IRA.
R GO; GO:0004896; F:mecptor activity; IEA.
R InterPro; IPR002996; CRIA.
R InterPro; IPR003932; Hemtopoptn S.F2.
R InterPro; IPR003332; Hemtopoptn S.F2.
R PROSITE; PS01356; HEMATOPO_REC_S_P2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 28, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
IL-13 receptor alpha 2 (Interleukin 13 receptor, alpha 2)
                                                                                                                                                                                                                                                                                                                                               Query Match
15.9%; Score 204.5; DB 11; Length
Best Local Similarity 25.6%; Pred. No. 4.6e-11;
Matches 60; Conservative 42; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                  385 AA; 44622 MW; EE06FF0E434737E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
```

```
142 KLSESQLELNWN---NRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 VENSIDIRMKWSTPGGPIPPRCYTYEIVIRED-DISW-ESATDKNDMKLKRRANESEDLC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 LOKKEIHL-YQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SDEGSLET-KIQDMKCIYYNWQYLVCSWKPGKTVYSDTNYTMFFWYEGLDH--ALQCADY 181
                                                                                                                                                                                                                                                                          LFSEEITSGCQLQKKEIHLYQTFVVQL--QDPREPRRQATQMLKLQNLVIPWAPENLTLH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 N--RFINHCLEHLVQY----RTD------WDHSWTEQSVDYRHKFSLPSVDGQKRY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 NPONFRSRCLTYEVEVNNTQTDRHNILEVEEDKCONSESDRNMEGTSCFPLPGVLADAVY 305
                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK082889; BAC38670.1; --
MGD; MGI:2147937; AI882074.
MGD; MGI:2147937; AI882074.
MGD; MGI:2147937; AI882074.
MGD; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
InterPro; IPR008957; FN III-like.
InterPro; IPR008957; FN III-like.
PROSITE; PS01356; HEMATOPOPT S F2.
PROSITE; PS01356; HEMATOPO REC S F2; 1.
SEQUENCE 424 AA; 48341 WW; E07ECBD276D67BB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Body;
MEDINES233546813; PLUMed=12466851;
The PANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVOCFVENVEYMICTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSH-YLPSEELTSGCQ
                                                                                                                                   25 IDSLSVSTLPLPBVQCFVFNVEYMNCTWN-SSSBPQPTNLTLHYWYKNSDNDKVQKCSHY
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                     11;
DB 11; Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
15.5%; Score 199.5; DB 11; 25.7%; Pred. No. 1.4e-10; Live 40; Mismatches 108;
```

Q8C1Z3

RESULT 13

```
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Kausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Shat N.K.,

RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Shat N.K.,

By Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

By Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toenlyuki S., Carninci P., Prange C.,

RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Mullahy S.J.,

RA Bosak S.A., McWan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

RA Achards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W.,

RA Halton D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.",

"Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 NPONFRSRCLIYEVEVNNTQTDRHNILEVEEDKCQNSESDRNWEGTSCFQLPGVLADAVY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 LOXKEIHL-YQTFVVOLODPREPRRQATQMLKLONLVIPWAPENLTLHKLSESQLEINWN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 BLKCIWHNLSYMKCSWLPGRNTSPDTHYTLYYWY--SSLEKSRQCENIYREGQHIACSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSH-YLFSEEITSGCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 N--RFINHCLEHLVQY---RID -----WDHSWTEQSVDYRHKFSLPSVDGQKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nome organica (unimaty). Buteleostomir. Salammala, Metrebrata, Euteleostomir. Salammala, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
10-CCT-2003 (TREMBLrel. 25, Last annotation update)
10-ECT-2003 (TREMBLrel. 18, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2002) to the RMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Strausberg R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC052425; AAH52425.1; -. Hypothetical protein. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 AA; 50128 MW; E2EF7C84C450661B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY; PRT; 427 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.1%; Score 181.5; DB 1
Best Local Similarity 27.6%; Pred. No. 8.2e-09;
Matches 56; Conservative 38; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 TVRVRVKTNKLCFDDNKLWSDWS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 TPRVRSRFNPLC-GSAQHWSEWS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 31-427 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawlor S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL13RA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96BB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 NPPNFRSRCITYEVEVNNTQTDRHNILEVEEDKCQNSESDRNMEGTSCFQLPGVLADAVY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 LOKKEIHL-YOTFVVOLODPREPRROATOMLKLONLVIPWAPENLTLHKLSESQLELNWN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 N--RFLNHCLEHLVQY---RTD-----WDHSWTEQSVDYRHKFSLPSVDGQKRY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK089984; BAC41028.1; -. MGD; MGI:2147937; AI882074. GO; GO:0016020; C:membrane; IEA. GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYYNSDNDKVQKCSH-YLFSEEITSGCQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium, the RANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Consortium of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCB_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mus musculus (mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.1%; Score 181.5; DB 11; Length 424; 27.6%; Pred. No. 7.8e-09; tive 38; Mismatches 86; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INCEMPRO: IPRO02996, CRRA.
INCEMPRO: IPRO08957; FN III-like.
INCEMPRO: IPRO08957; FN III-like.
INCEMPRO: IPRO08952, Hemicopoptin S.F2.
SEQUENCE: 424 AA, 48371 WW. 4845BBBBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Tremblrel. 25, Created)
(Tremblrel. 25, Last sequence update)
(Tremblrel. 25, Last annotation update)
                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 TVRVRVKTNKLCFDDNKLWSDWS 328
       306 TVRVRVQTNKLCPDDNQLWSDWS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFRVRSRFNPLC-GSAQHWSEWS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN=CS7BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein (Fragment) Mus musculus (Mouse).
                                                                                                                                                                                      (TrEMBLrel. 23, (TrEMBLrel. 23, TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy
nes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel.
Interleukin 13 receptor.
AI882074.
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                        01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

Matches

셤

ð

ઠ

ò 셤 ð Q7TT27

ACCOCCOSE REPRESENTATION OF THE PROPERTY OF TH

RESULT 14

9

23;

301 GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIG 337

learch completed: March 3, 2004, 12:38:06
fob time : 39.9085 secs

OM protein - protein search, using sw model

Run on:

Copyright (c) 1993 - 2004 Compugen Ltd. Copyright (c) 1993 - 2004 Compugen Ltd. Copyright (c) 1993 - 2004 Compugen Ltd. Copyright (c) 1993 - 2004 Compugen Ltd. Standard C			26	1272	98.8	230	64	AAR82934	
29 853.5 66.3 369 5 30 542 42.1 121 3 31 542 42.1 121 3 32 215 16.7 561 4 33 215 16.7 561 4 34 215 16.7 561 4 35 215 16.7 563 4 36 213 16.5 318 4 37 213 16.5 318 4 38 213 16.5 318 4 39 207 16.1 315 2 41 207 16.1 380 2 42 207 16.1 380 2	н		28	854.5	•	369	r (1)	AAR59094	
30 542 42.1 121 3 31 542 42.1 121 3 32 5.3464 Seconds 33 215 16.7 561 4 34 215 16.7 561 4 35 215 16.7 561 4 36 213 16.5 318 4 37 213 16.5 318 4 38 213 16.5 318 4 39 207 16.1 315 2 41 207 16.1 380 2 44 207 16.1 380 2 45 207 16.1 380 2			29	853.5	_	369	Ŋ	AAU77221	
31 542 42.1 121 6 32 215 16.7 561 4 33 215 16.7 561 4 34 215 16.7 561 4 35 215 16.7 561 4 36 213 16.7 563 4 37 213 16.5 318 4 38 213 16.5 318 4 39 207 16.1 317 5 41 207 16.1 380 2 44 207 16.1 380 2			30	542	•	121	m	AAG00283	
355.3464 Seconds 355.3464 Seconds 36 215 16.7 561 4 37 215 16.7 561 4 38 215 16.7 563 4 39 215 16.7 565 4 37 213 16.5 318 4 38 213 16.5 318 4 39 207 16.1 315 2 41 207 16.1 380 2 42 207 16.1 380 2 44 207 16.1 380 2 45 207 16.1 380 2			31	542	•	121	ø	ABU03604	
55.3464 Seconds 33 215 16.7 561 4 34 215 16.7 563 4 34 215 16.7 563 4 35 215 16.7 563 4 36 213 16.5 318 4 37 213 16.5 318 4 39 207 16.1 315 2 41 207 16.1 380 2 44 207 16.1 380 2 44 207 16.1 380 2			32	215	•	561	4	AAU69138	
### 15 10 10 10 10 10 10 10	ne 55.3464 Seconds	-	33	215	٠.	561	4	AAU69141	
110n cell updates/sec 35 215 16.7 565 4 36 213 16.5 318 4 37 213 16.5 318 4 37 213 16.5 318 4 38 213 16.5 318 4 38 213 16.5 386 4 39 207 16.1 315 2 41 207 16.1 319 2 42 207 16.1 380 2 44 207 16.1 380 2 44 207 16.1 380 2 44 207 16.1 380 2 45 207 16.1 380 2	alignments)		34	215	•	563	4	AAU69140	
232 36 4 37 213 16.5 346 4 38 213 16.5 365 4 39 207 16.1 315 2 40 207 16.1 315 2 41 207 16.1 390 2 42 207 16.1 380 2 44 207 16.1 380 2 45 207 16.1 380 2	lion cell		35	215	•	565	4	AAU69139	
232 36 4 232 20 16.5 366 4 39 207 16.1 315 5 40 207 16.1 317 5 41 207 16.1 389 2 43 207 16.1 380 2 44 207 16.1 380 2 45 207 16.1 380 2			36	213	•	318	4	AAU69137	
38 213 16.5 386 4 39 207 16.1 315 2 40 207 16.1 315 2 41 207 16.1 359 2 42 207 16.1 380 2 44 207 16.1 380 2 45 207 16.1 380 2			37	213	• •	365	4	AAU69136	
232			38	213	•	386	4	AAU69135	
16.1 317 5 16.1 359 2 16.1 380 2 16.1 380 2 16.1 380 2 16.1 380 2	EWSHPIHWGSNTSKEN 232		39	207	•	315	N	AAW56261	
16.1 359 2 16.1 380 2 16.1 380 2 16.1 380 2 16.1 380 2			40	207	•	317	ហ	AAE13746	
16.1 380 2 1 16.1 380 2 1 16.1 380 2 1 16.1 380 2 2 1 16.1			41	207	•	359	N	AAW56260	
16.1 380 2 7 16.1 380 2 7 16.1 380 2 7		•	42	207	•	380	Ŋ	AAW36613	
16.1 380 2 P			43	207	•	380	N	AAW35295	
16.1			44	207	•	380	7	AAW24972	
			45	207	•	380	N	AAW33603	

Human, Zalphall, cytokine receptor; immunosuppressive; cytostatic; inflammatory disorder; haemostatic; cell proliferation; immune disorder; autoimmune disease; rheumatoid arthritis; multiple solerosis; cancer; myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma; ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis; viral infection; IL-2Rgamma. Human soluble IL-2Rgamma cytokine receptor protein fragment. AAE13727 standard; protein; 232 AA (first entry) 26-FEB-2002 AAE13727; RESULT 1 AAB1372

Homo sapiens.

18-OCT-2001.

WO200177171-A2.

03-APR-2001; 2001WO-US010872

05-APR-2000; 2000US-0194731P. 28-JUL-2000; 2000US-0222121P.

(ZYMO) ZYMOGENETICS INC.

West JW, Presnell SR, Holly RD, Nelson AJ;

WPI; 2002-025898/03. N-PSDB; AAD22919.

Sprecher CA, Novak JE,

Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune response in a mammal.

Claim 29; Page 175-176; 243pp; English

The invention relates to an isolated soluble ralphall cytokine receptor polypopide and their colM molecules ralpha proteins are useful for inhibiting or antagonising the ligand activity-induced proliferation of haematopoletic cells and haematopoletic cell progenitors preferably lymphoid cells which are natural killer cells or cytokoxic Tesls. Tapha is useful for treating immune and inflammatory disputers; for reducing proliferation of neoplastic B or T cells, for suppressing an

	26	1272	98.8	230	N		Aar82934	Interle
	27	960	74.5	363	4	AAB71682 Aa	Aab71682	Bos tau
-	28	854.5	66.3	369	N		Aar59094	Murine
	29	853.5	66.3	369	Ŋ	AAU77221 Aa	Aau77221	Mouse o
-	30	542	42.1	121	m	AAG00283 Aa	Aag00283	Human s
	31	542	42.1	121	ø	ABU03604 Ab	Abu03604	Human e
	32	215	16.7	561	4	AAU69138 Aa	Aau69138	Canine
	33	215	16.7	561	4	•	Aau69141	Canine
	34	215	16.7	563	4		Aau69140	Canine
	35	215	16.7	565	4		Aau69139	Canine
	36	213	16.5	318	4		Aau69137	Canine
	37	213	16.5	365	4	AAU69136 Aa	Aau69136	Canine
	38	213	16.5	386	4		Aau69135	Canine
	39	207	16.1	315	Ŋ		Aaw56261	Mature
	40	207	16.1	317	Ŋ		Aae13746	Human 8
	41	207	16.1	359	N	AAW56260 Aa	Aaw56260	Constru
,	42	207	16.1	380	ď	AAW36613 Aa	Aaw36613	Human 2
	43	207	16.1	380	N	AAW35295 Aa	Aaw35295	Human I
	44	207	16.1	380	~	AAW24972 Aa	Aaw24972	Human i
	45	207	16.1	380	N	AAW33603 Aa	Aaw33603	Ното ва

ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A_Geneseq_29Jan04:*

Database

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Scoring table:

score:

Sequence:

geneseqp1990s:* geneseqp2000s:* geneseqp1980s:* geneseqp2001s:*

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aae13727 Human sol	0	Aar47149 IL-2 rece	9 IL-2	Aael3734 Human sol	Aar47148 IL-2 rece	Aau96932 Human cyt	Abu03612 Human exp	Human	Abu03602 Human exp		Abu03605 Human exp	Abu03600 Human exp	Нишап	2 Fusior	Human	Fusior	Fusion	Human e	Abu03609 Human exp	Aaw31646 Human cyt	Abu03608 Human exp	н	Aar47150 IL-2 rece	Abu03606 Human exp
SUMMARIES	ID	AAE13727	ABR61610	AAR47149	ABR61609	AAE13734	AAR47148	AAU96932	ABU03612	ABU03613	ABU03602	ABU03603	ABU03605	ABU03600	ABU03601	AAY92202	ABU03610	AAY92201	AAY92203	ABU03611	ABU03609	AAW31646	ABU03608	AAR47151	AAR47150	ABU03606
	DB	2	7	7	7	S	~	ß	ø	9	9	ø	9	9	9	ო	9	m	m	φ	9	N	φ	N	N	9
	Length	ľ	4	4	S	9	φ	9	Q	φ	9	369	9	ø	9	σ	6	σ	σ	O)	694	482	σ	n	252	ഗ
	% Query Match	10	100	100	Н	100	100.0	100.	Н	100.	100.	100.	100.	Н	100.	100	100.	Н	100.	100.	-	99.	99.	99	99	99.1
	Score	122	$^{\circ}$	N	N	N	$^{\circ}$	$^{\circ}$	α	N	$^{\circ}$	1288	N	N	α	N	ď	N	N	N	N	N	N	N	N	1277
	Result No.		7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

```
ö
                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                     TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                          TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOMLKLONLVI PWAPENLTLHKLSESOLBLNWNNRFLNHCLEHLVQYRTDWDHSWTEOSV 180
immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes; asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, sepsis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble IL-Rgamma cytokine receptor CDNA fragment
                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                             1 INTILLTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal; antiarthrific; antirheumatic; osteopathic; cardiant;
antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic;
immunosuppressive; antithyroid; nuclear factor kB inducing kinase; NIK;
                                                                                                                                                                                                                                                            1 LATTILIPNGNEDITADFFLTTMPTDSLSVSTLPLPEVOCFVFNVBYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                    TNLTLHYWYKNSDNDKVOKCSHYLFSEEITSGCOLOKKEIHLYOTFVVOLODPREPRROA
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New interleukin-2 common gamma chain or its mutein, variant, fusion protein, functional derivative, circularly permutated derivative or fragment useful for treating Alzheimer's disease or atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin 2; common gamma chain; cgammac; antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                       ö
                                                                                                                                                                                  100.0%; Score 1288; DB 5; Length 232; 100.0%; Pred. No. 3e-115; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-2 common gamma chain (cgammac) fragment (residues 1-341).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shmushkovich T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 97-98; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR61610 standard; peptide; 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-2003; 2003WO-IL000316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2002; 2002IL-00149217.
08-OCT-2002; 2002IL-00152183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wallach D, Ramakrishnan P,
                                                                                                                                                                                                      Best Local Similarity 100 Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-845330/78.
                                                                                                                                                 Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003087374-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR61610;
                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR61610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
   888888888888
                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

The invention relates to an interleukin 2 (IL-2) common gamma chain (ogammac) or its mutein, variant, fusion protein, functional derivative, circularly permutated derivative or fragment. Specific antibodies and

```
small molecules capable of modulating the interaction between IL-2 cgammac and nuclear factor kB inducing kinase (NIK) are useful for the manufacture of a medicament for the treatment of a disease, e.g. a disease resulting from excessive immune response such as rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, asthma, cardiac infarct, Alzheimer's disease or atherosclerosis; or an autoimmune disease, such as immune thyroiditis, or other arthropaties, e.g. autoimmune haemolytic anemia. The small molecule is useful for modulating signaling through cgammac. The present sequence represents an IL-2 cgammac protein
                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                                  121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                   TNLTLHYWYKNSDNDKVOKCSHYLFSEEITSGCOLOKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                 83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                              143 TOMIKIONIVIPWAPENLTIHKISESQLEINWANRFINHCLEHLVOYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                              1 LNTTILIPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                 23 INTILITPNGNEDITADFFLITMPIDSLSVSTLPLPERVQCFVFNVBYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA and protein sequences of IL-2 gamma chain - useful as immune regulatory agents for treatment of e.g. rheumatoid arthritis and transplant rejection.
                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimamura T;
                                                                                                                                                                                                                 Length 341;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-2 receptor gamma chain; IL-2; receptor; rheumatoid arthritis; transplant rejection; primer; polymerase chain reaction; PCR; amplification.
                                                                                                                                                                                                                 100.0%; Score 1288; DB 7;
100.0%; Pred. No. 5.2e-115;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takeshita T, Asao H, Nakamura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR47149 standard; protein; 347 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92JP-00104947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 41; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93EP-00106561:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-2 receptor gamma chain.
                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamuro J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-017546/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUGA/) SUGAMURA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ54829.
                                                                                                                                                                                   Sequence 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugamura K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
13-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP578932-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suzuki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR47149;
                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                   fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8888888888888
                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                                                                                                                                                     ठ
```

\$\$888888888888**\$**8

The human IL-2 receptor gamma chain preform (AAR47148), including the signal peptide, is encoded by the sequence given in AAQ54828. The mature protein (AAR47149) is encoded by sequence AAQ548319, while a soluble form of IL-2 receptor gamma chain (AAR47150) is encoded by AAQ548310, while a soluble form suitable for expression in prokaryotes (AAR47151) is encoded by AAQ548310. Primers 1-6 (AAQ54820-25) are based on the N- terminal sequence of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma chain, and are used to isolate IL2 receptor gamma given in AAR47151. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 347 AA;

TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDFREPRRQA 120 180 121 TOMIKIONIVIPWAPENITIHKISESQIEINWNNRFINHCLEHLVQYRTDWDHSWTEGSV 180 LNTILLTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP TOMIKLONLVI PWAPENI TLHKLSESQLEINWNNRFINHCLEHLVOYRTDWDHSWTEQSV LNTIILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP Gaps 232 ö DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN Length 347; Indels 100.0%; Score 1288; DB 2; 100.0%; Pred. No. 5.3e-115; ive 0; Mismatches 0; Best Local Similarity 100. Matches 232; Conservative 67 121 19 181 181 Query Match ò 임 ઠે 음 ઠ 셤

ABR61609 RESULT

ABR61609 standard; peptide; 357 ABR61609;

(first entry) 15-JAN-2004

common gamma chain (cgammac) fragment (residues 1-357). IL-2

IL-2; interleukin 2; common gamma chain; cgammac; antiinflammatory; gastrointestinal; antiarthritic; antirheumatic; osteopathic; cardiant; antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic; immunosuppressive; antithyroid; nuclear factor kB inducing kinase; NIK; gene therapy

sapiens Ношо

WO2003087374-A1

23-OCT-2003

15-APR-2003; 2003WO-IL000316.

2002IL-00149217. 2002IL-00152183. 18-APR-2002; 08-OCT-2002;

(YEDA) YEDA RES & DEV CO LTD

Ramakrishnan P, Shmushkovich T; Ö, Wallach

WPI; 2003-845330/78.

New interleukin-2 common gamma chain or its mutein, variant, fusion protein, functional derivative, circularly permutated derivative or fragment useful for treating Alzheimer's disease or atherosclerosis.

Page 96-97; Opp; English Claim 5;

(ggammac) or its mutein, variant, function protein, functional derivative, circularly permutated derivative or fragment. Specific antibodies and carcularly permutated derivative or fragment. Specific antibodies and cgammal molecules capable of modulating the interaction between IL-2 cyammac and nuclear factor kB inducing kinase (NIK) are useful for the manufacture of a medicament for the treatment of a disease, e.g. a disease resulting from excessive immune response such as rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, asthma, cardiac such as immune thyroiditis, or ther arthropaties; e.g. autoimmune disease haemolytic anemia. The small nolecule is useful for modulating signaling through cgammac. The present sequence represents an IL-2 cgammac protein 120 142 180 202 9 82 23 INTTILIPNGNEDITADFFLITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 121 TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 143 TOMIKLONIVIPWAPENLILIKILSESQLEINWNNRFINHCLEHIVOYRIDMDHSWTEQSV 1 INTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP ô Length 357; Indels 100.0%; Score 1288; DB 7; 100.0%; Pred. No. 5.5e-115; invention relates to an interleukin 2 (IL-2) ö 0; Mismatches Matches 232; Conservative Local Similarity Sequence 357 AA; 61 Query Match 8\$388888888888888 셤 셤 셤 ò ઠ ઠ

ö

9 9 RESULT 5

AAE13734 standard; protein; 360 AA;

203

셤 ò

181

DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN

(first entry) 26-FEB-2002

Human soluble IL-2Rgamma/kappa light chain chimeric DNA construct

Human, Zalphall, cytokine receptor, immunosuppressive; cytostatic; inflammatory disorder, haemostatic; cell proliferation, immune disorder, autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma; ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis; viral infection; fusion protein; IL-ZRgamma.

Homo sapiens.

WO200177171-A2.

18-OCT-2001

03-APR-2001; 2001WO-US010872.

05-APR-2000; 2000US-0194731P. 28-JUL-2000; 2000US-0222121P.

(ZYMO) ZYMOGENETICS INC.

98. THE

Ż Nelson Presnell SR, Holly West JW, Ę Sprecher CA, Novak

WPI; 2002-025898/03. N-PSDB; AAD22926.

Novel soluble receptor polypeptides and polynucleotides used as cytokine

```
(AJIN ) AJINOMOTO KK. (SUGA/) SUGAMURA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JAK3; c
human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
        쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 TOMIKLONLVIPWAPENLILHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                    The invention relates to an isolated soluble zalphall cytokine receptor polypeptide and their cDNA molecules. Zalpha proteins are useful for inhibiting or antagonising the ligand activity-induced proliferation of haematopoletic cells and haematopoletic cells progenitors preferably lymphoid cells which are natural killer cells or cytotoxic T cells. Is useful for treating immune and inflammatory disorders, for reducing proliferation of neoplastic B or T cells, for suppressing an immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthritis, multiple solerosis, myasthenia gravis, systemic lupus erythematosus (SLB) and diabetes; sethum, ulcerative colitis, inflammatory bowel disease. Crohn's disease, sepsis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble IL-2Rgamma/kappa light chain fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 INTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 INTTILTPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator; rheumatoid arthritis; transplant rejection; primer; PCR; polymerase chain reaction; amplification; ss.
    antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune response in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1288; DB 5; Length 360; 100.0%; Pred. No. 5.6e-115; ive 0; Mismatches 0; Indels 0
                                                                                                                                       Example 28; Page 196-197; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .22
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR47148 standard; protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93EP-00106561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92JP-00104947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-2 receptor gamma chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
13-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP578932-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR47148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR47148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \mathbb{E}\,\mathbb{E}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde{\mathbf{x}}\,\tilde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
The human IL-2 receptor gamma chain preform (AAR47148), including the signal peptide, is encoded by the sequence given in AAG54828. The mature protein (AAR47149) is encoded by sequence AAG54829. A soluble form of IL-2 receptor gamma chain (AAR47150) is encoded by AAG54830, while a soluble form suitable for expression in prokaryotes (AAR47151) is encoded by AAG54831. Primers 1-6 (AAG54820-25) are based on the N- terminal sequence of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma chain, and are used to obtain the protein given in AAR47151. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 TNLTLHYWYKNSDNDKVQKCSHYLFSEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; immunomodulatory; antiinflammatory; graft rejection; antirheumatic; infection; hypogammaglobulinaemia; SCID; Combined Immunodeficiency; Janus kinase; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 INLILHYWYKNSDNDKVQKCSHYLFSBEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 TOMIKLONLVIPWAPENLILHKUSESQLELNWNNRFLNHCLEHLVQYRIDWDHSWIEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 INTILLTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYNNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 INTTILIPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 DYRHKFSIPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                         DNA and protein sequences of IL-2 gamma chain - useful as immune regulatory agents for treatment of e.g. rheumatoid arthritis and transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1288; DB 2; Length 369; Best Local Similarity 100.0%; Pred. No. 5.8e-115; Matches 232; Conservative 0; Mismatches 0; Indels 0;
Asao H, Nakamura M, Shimamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis; autoimmunity; gamma chain
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 16-17, 29-30; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytokine receptor common gamma chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU96932 standard; protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-00191786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00191786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
       Takeshita T,
   Sugamura K, Takeshi
Suzuki M, Hamuro J;
                                                                                                            WPI; 1994-017546/03.
                                                                                                                                                 N-PSDB; AAQ54828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6372898-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU96932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
```

Cacalano NA, Johnston JA;

WPI; 2002-433679/46

(SCHE) SCHERING CORP.

```
This invention relates to a novel isolated human Jak3 variant polynucleotides. The Jak3 or gamma c polypeptides, muteins, fragments, polynucleotides to them are useful For in vitro or in vivo screening or treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions and severe infections due to reduced levels of T and natural killer (IMK) cells, as well as hypogammaglobulinaemia. The kinases suggests the possibility of biological activities beyond the Severe Combined Immunodeficiencies described patients with specific mutations in either the gamma c subunit of a cytckine receptor (e.g., IL-4, IL-7, IL-9, and IL-15) or in the Janus kinase. In particular, modulation of Jak kinase activities should be useful in situations where the Jak kinase activities should be useful in situations where the Jak kinase activities should be useful in situations where the Jak kinase activities should be useful in situations where the Jak kinase activities should be useful in situations where the Jak kinase activities should be useful in situations where the Jak kinase thuctions have been implicated, e.g., lymphoid cell degeneration, and atrophy of responsive cell types: For example, and strophy of responsive cell types: The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 INLILHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOMLKLONLVI PWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Translational profiling, expressed protein tag, EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 INTILITPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 TOMIKLONLVIPWAPENLTLHKLSESQIELNWNNRFLNHCLEHLVOYRTDWDHSWTEGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LINTIILTPNGNEDITADFFLITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
variant polynucleotides useful for preventing, diagnosing and ing e.g. cancers, inflammation and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represents the human cytokine receptor common gamma chain protein sequence used to identify regions of JAK3 that are important for interaction with the common gamma chain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYRHKFSLPSVDGOKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1288; DB 5; Length
100.0%; Pred. No. 5.8e-115;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human expressed protein tag (BPT) #278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU03612 standard; protein; 369 AA
                                                                                                                                               Example; Col 9-11; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 369 AA;
                                                        treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU03612;
Jak3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ਨੋ
```

The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease, inhibitor, transporter, cytosketatal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to polypeptide, is useful for treating cancer. The polypeptide is also polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed polymenides are particularly useful for treating or preventing myelona, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, imphona or leukaemia. These are also useful for greening agents for treating the above mentioned diseases. This sequence represents an expensed protein tag (RFT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed profiling. When the published byte sequences to appear in the printed profiling. Note: This sequences are also appear in the printed profiling. Note: This sequences does not appear in the printed profiling. Note: This sequences are also appear in the printed profiling. Note: This sequences are also appear in the printed profiling. Note: This sequences are also appear in the printed profiling. Note: This sequences are also appear in the printed profiling. Note: This sequences are also appear in the printed profiling. Note: This sequences are also appear in the printed profiling. Note: This sequences are also appear in the printed profile and appear are appeared profile and appear are appeared and appeared and appeared and appeared and appeared and appeared appeared and appeared and appeared and appeared and appeared and appeared and appeared and appeared appeared and appeared appeared and appeared appeared and appeared appeared and appeared appeared and appeared appeared and appeared appeared appeared appear 61 TNLTLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKEIHLYQTFVVQLQDPREPRQA 120 cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or 143 TOWLKLONLVIPWAPENLTLAKLSESQLELNWNNRFLANGLEHLVOYRTDWDHSWTEQSV 1 INTILITPNGNEDITADFFLITMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 23 INTTILTENGNEDITADFFLITMPTDSLSVSTLPLPEVOCEVENVEYMNCTWNSSSEPQP TOMIKLONIVI PWAPENLTLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 0; Gaps DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232 DYRHKFSLPSVDGOKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254 Length 369; 0; Indels Mouery Match

Mest Local Similarity 100.0%; Pred. No. 5.88-115;

Matches 232; Conservative 0; Mismatches 0; polypeptides (e.g. kinases, phosphatases, Example 2; SEQ ID NO 278; 134pp; English Tomlinson AJ, Urban RG; 21.MAY-2001; 2001US-0292544P. 08-AUG-2001; 2001US-0310801P. 01-CT-2001; 2001US-032570P. 20-FEB-2002; 2002US-03589B5P. 28-MAR-2002; 2002WO-US009671 WPI; 2003-040607/03. (ZYCO-) ZYCOS INC. Sequence 369 AA; WO200278524-A2 Homo sapiens. 10-OCT-2002 Chicz RM, 83 121 181 ର ନ à 120 82

9

ABU03613 standard; protein; 369 AA

ABU03613 RESULT

phosphatase;

ABU03613;

```
The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic composition for eliciting in a mammal an immunogenic composition for eliciting in a colypeptide. The purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide is useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptide and class I or class II MHC-binding polypeptide. The polypeptides and class I or leukamia. These are also useful for reating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, asrcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence fores represents an texting the above mentioned diseases. This sequence fore represents an profiling. Note: This sequence does not appear in the printed profilation but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                      Translational profiling, expressed protein tag; EPT; kinase; phosphatase; protease inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
TOMIKLONLVIPWAPENLTLHKLSESQLEINWINRFINHCLEHLVQYRTDWDHSWTEQSV 180
                        143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEGSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                               DYRHKESLESVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 268; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                   Human expressed protein tag (EPT) #268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urban RG;
                                                                                                                                                                                                                               ABU03602 standard; protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001; 2001US-0279495F.
21-MAY-2001; 2001US-0292544F.
08-AUG-2001; 2001US-0310801P.
04-DEC-2001; 2001US-0326370F.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2002; 2002WO-US009671.
                                                                                                                                                                                                                                                                                                              29-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-040607/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200278524-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicz RM,
                                                                                                                                                                                                                                                                      ABU03602;
                                                                                                                            203
      121
                                                                                     181
                                                                                                                                                                                                                ABU03602
                                                                                                                                                                                                                                   ò
                                                                                                                        g
```

Sequence 369 AA

TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDFREFRRQA 120 83 INLILHYWYRASDNDKVQKCSHYLFSBEITSGCQLQKKEIHLYQTFVVQLQDPREPRRA 142

19

23 INTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVOCFVFNVEYMNCTWNSSSEPQP 82

1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP

100.0%; Score 1288; DB 6; 100.0%; Pred. No. 5.8e-115; ive 0; Mismatches 0;

232; Conservative

Similarity

ö

Gaps ö

Length 369; Indels

ઠે g d

ઠે

요

ઠે

d

ઠે

```
29-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-040607/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYCO-) ZYCOS INC.
                                                                                                                                                             Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200278524-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2001;
20-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-CCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicz RM,
                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU03605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88888888888
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor. Transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide is useful for tracting oracer. The polypeptide is useful for tracting cancer. The polypeptide is also useful for tracting cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed
                                                                                                                              120
                                                                                                                                                             142
                                                                                                                                                                                            180
                                                                                                                                                                                                                           TOWLKLONLVIPWAPENLTLHKLSESOLEINWNNRFLNHCLEHLVOYRTDWDHSWTEGSV 202
                                                                 9
                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability cancer; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma cleukemia.
                                                                                  LINTILLTPNGNEDTTADFFLTTMPTDSLSVSTLFLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                            TNLTLHYWYKNSDNDKVQKCSHYLFSBBITSGCQLQKKBIHLYQTFVVQLQDPRBPRRQA
                                                                                                                                                           TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                            TOMIKLONLVI PWAPENLTLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                               1 LNTTILIPNGNEDITADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                   Gapa
                                ;
0
                                                                                                                                                                                                                                                                              DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                           DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
   Length 369;
                                Indels
Score 1288; DB 6;
Pred. No. 5.8e-115;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 269; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human expressed protein tag (EPT) #269
                                                                                                                                                                                                                                                                                                                                                                         ABU03603 standard; protein; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2001, 2001US-0279495P.
21-MAY-2001, 2001US-0292544P.
08-AUG-2001, 2001US-0310801P.
01-OCT-2001, 2001US-0326370P.
04-DEC-2001, 2001US-0336780P.
20-FEB-2002, 2002US-0358985P.
 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002; 2002WO-US009671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicz RM, Tomlinson AJ,
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-040607/03.
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200278524-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2003
                                232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2002
                                                                                                                            61
                                                                                                                                                           83
                                                                                                                                                                                            121
                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                          203
 Query Match
Best Local (
               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                           ABU03603
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Translational profiling, expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
class I or class II MHC-binding polypeptide. The polypeptides and polynuclectides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNTTILTPNGNEDTIADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSERQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 TOMLKLONLVIPWADENLTLHKLSESOLEINWNNRFINHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNLTLHYWYKNSDNDKVQKCSHYLFSERITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 TNLTLHYWYKNSDNDKVQKCSHYLFSEBITSGCQLQKKEIHLYQTFVVQLQDPREPRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMIKI ONLVI PWAPENLTLHKI SESOLELNWNNRFLNHCLEHLVOYRTDWDHSWTEOSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1288; DB 6; Best Local Similarity 100.0%; Pred. No. 5.8e-115; Matches 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed protein tag (EPT) #271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU03605 standard; protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 2001US-0279495E.
, 2001US-0292544E.
, 2001US-0310801P.
; 2001US-0326370E.
; 2001US-0336780E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2002; 2002WO-US009671.
```

leukemia

```
The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor our transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I will make binds to a naturally processed polymolectides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, machanic myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translational profiling, expressed protein tag, EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOMIKLONIVI PWAPENI TIHKUSESQLEINWNNRFINHOLEHLVOYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYRHKESLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1288; DB 6;
100.0%; Pred. No. 5.8e-115;
tive 0; Mismatches 0;
                                   Example 2; SEQ ID NO 271; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human expressed protein tag (EPT) #266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU03600 standard; protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUC 2001; 2001US-0310801P.
01-OCT-2001; 2001US-031681P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2002; 2002WO-US009671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200278524-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L0-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU03600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU03600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ч
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

202

82

Gaps

```
The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide is useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, reating or preventing englowed protein tages. This sequence represents an treating the above mentioned diseases. This sequence represents for treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed profiling to but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TOMIKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 İNLILLAYWYKNSDNDKYOKCSHYLFSERITSGCÖLÖKKEIHLYQIPVVOLODPREPRROA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melmanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 INTILLIPHINGNEDITADPELITHPIDSLSVSTLPLPERVQCFVFNVEXMNCTWNSSSEPQP 82
                                                                                                                                                                                           New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LNTTILTPNGNEDITADFFLTTMPIDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 DYRHKESLPSYDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1288; DB 6; Length 369; 100.0%; Pred. No. 5.8e-115; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 266; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human expressed protein tag (BPT) #267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU03601 standard; protein; 369 AA
                                                                                                            Urban RG
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232; Conservative
                                                                                                            Tomlinson AJ,
                                                                                                                                                  WPI; 2003-040607/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 232; Conserv
                                                                  (ZYCO-) ZYCOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2003
                                                                                                          Chicz RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

ö

თ

```
This sequence shows fusion polypeptide 603, which is capable of binding cytokine IL-4 to form a non-functional complex. The invention concerns production of antagonists to any cytokine that utilizes an alpha production of antagonists to any cytokine that utilizes an alpha pecificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sR alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (sR-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokien to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (dillary ineurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, considering of the ligand, it will effectively block the action of the ligand. Effective antagonists of little considering expensive and its beta-1 receptor component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specificity determining components of their receptors and the extracellular domain of gpi30. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessbile to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders section as esteoporosis and primary and secondary effects of cancer including multiple myeloms or cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex.
                                                                                                                                                    antagonist; CNTF; receptor; fusion protein;
                                                                                                                                                                               cytostatic, immunomodulator, osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Fig 22A-D; 152pp; English.
                                                                                               Fusion polypeptide 603, IL-4 trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 232; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0101858P.
99US-00313942.
                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US022045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGE-) REGENERON PHARM INC.
                                                 01-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yancopoulos GD;
                                                                                                                                                    IL-4 trap; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-293165/25.
N-PSDB; AAA09044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 691 AA;
                                                                                                                                                                                                                                                                                                          WO200018932-A2
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                               06-APR-2000
                                                                                                                                                                                                                                Synthetic.
AAY92202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stahl N,
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor. transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in ammanda an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to polypeptide, is useful for treating cancer. The polypeptide is also useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to ancurately processed class I or class II MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational spocifiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNLTLHYWYKNSDNDKVQKCSHYLPSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNLTLHYWYKNSDNDKVQKCSHYLPSEIITSGCQLQKKBIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSFPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOMLKLONLVI PWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVOYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOMIKLONLVI PWAPENLTLHKISESOLELNWNNRPLNHCLEHLVOYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1288; DB 6; Length 369; 100.0%; Pred. No. 5.8e-115; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 267; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Urban RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY92202 standard; protein; 691 AA
                                                                                                                                                                                                                              2001US-0292544P.
2001US-0310801P.
2001US-0326370P.
2001US-0336780P.
                                                                                                                                                    28-MAR-2002; 2002WO-US009671
                                                                                                                                                                                                                                                                                                                                2002US-0358985P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicz RM, Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-040607/03
                                                                                                                                                                                                                                                                                                                                                                                    (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 369 AA;
                                                 WO200278524-A2
                                                                                                                                                                                                                                                                            01-OCT-2001;
04-DEC-2001;
20-FEB-2002;
Homo sapiens.
                                                                                                                                                                                                     28-MAR-2001;
                                                                                                                                                                                                                                                      08-AUG-2001;
                                                                                               10-OCT-2002
                                                                                                                                                                                                                              21-MAY-2001
```

Leukemia

23 61

à

121 143 181 203

à

ద ð 셤

g

8

RESULT 15
AAY92202
ID AAY922

```
120
                                                                                   9
                                                                                                                                                                       TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                      1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                             23 INTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVBYMNCTWNSSSEPQP
                                         0; Gaps
Length 691;
Score 1288; DB 3; Length
Pred. No. 1.4e-114;
0; Mismatches 0; Indels
                                                                                                                                                                            61
```

```
83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
```

180	202
121 TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180	143 TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
121	143

ò

ď

음

ò a

Search completed: March 3, 2004, 12:35:37 Job time : 57.3464 secs

```
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9hbe4 homo sapien
Q9es17 mus musculu
Q80xg2 peromyscus
Q80xg2 peromyscus
Q8d6p4 vibrio vuln
Q8dis6 synechococc
Q82333 salmonella
Q5237 salmonella
Q5227 shigella so
Q8cpt9 staphylococ
Q9ve8 drosophila
Q917 drosophila
Q917 drosophila
Q9660 dictyoseeli
Q9k60 drosophila
Q9k60 drosophila
Q9nk60 drosophila
                                                                             March 3, 2004, 12:31:14; Search time 26.4706 Seconds (without alignments) 1930.971 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       1 MRSSPGNMERIVICLMVIFL......LLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                     1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09ES17
08DS14
08DSP4
08DJS6
08DJS6
08Z39
08Z39
08CPT9
08CPT9
08CPT9
08CPT9
08CPT9
08CPT9
08CPT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pplant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_rvirus:*
                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9HBE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organelle:*
phage:*
                                                                                                                                                                                                                                                                                                  Winimum DB seg length: 0 Maximum DB seg length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                 sp_archea:*
sp_bacteria:*
                                                                                                                                        US-09-825-561A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_human: *
                                                                                                                                                                                                                                                                                                                                                                                                                                              fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_mhc:*
sp_organe
sp_phage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        850
486
392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.5
83.5
83.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.5
                                                                                                                                           litle:
Perfect score:
                                                                                                                                                                                                  scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                     Jatabase :
                                                                                                                                                                          sequence:
                                                                                                                                                                                                                                           Searched:
                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
```

Q81k96 plasmodium Q9w756 gallus gall Q91y09 ums musculu Q80w92 mus musculu Q8euw0 mycoplasma Q8ema4 drosophila Q91j48 mus musculu Q7xxp8 oryza sativ Q8f14 homo sapien Q8wyp0 homo sapien Q8wyp0 drosophila Q20239 calliphora Q9w3h8 drosophila Q9w3h8 drosophila Q8wx22 drosophila Q8wx23 drosophila Q8wx23 drosophila Q8wx24 drosophila Q8wx25 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q8wx26 drosophila Q9w3h6 drosophila Q9w3h6 drosophila Q9w3h6 drosophila Q9w3h6 drosophila Q9w3h6 drosophila	∞ ⊣
QBIK96 Q9W756 Q9W756 Q80X90 Q80X90 Q80X00 Q80X00 Q9XJ48 Q7XV89 Q7XV89 Q9WX82 Q9WX83 Q09WX83 Q09WX85	Q22975 Q8K5L8 Q8ELA1 Q86K11 Q8IRP4 Q8I3M4 Q8I119
84446 40 88 88 88 88 88 88 88 88 88 88 88 88 88	សក្ស
4638 1872 1873 1873 1873 1873 1873 1873 1873 1873	04 08 08 08 08 08 08 08 08 08 08 08 08 08
80	**************************************
	W W 4 4 4 4 4 4 8 8 9 9 9 9 11 8 11 8 14 15

ALIGNMENTS

													_			•	:	Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,		n and										Gaps	
							jmi;	Catarrhini; Hominidae; Homo.				MEDLINE=20531754; Pubmed=11081504;	i i			ly X	ert	:	•	ngio											
							ost					٠.	che:	er		Que :	Ρ̈́	e E		x Da									2 ;	0;	
							ele	οщο ·				5	pre	rad	٠. تا	Ξ		TOU:											1 16	8	
							But	Ħ,				,	:	SCL	ame	υ Ω	ں ح	M		e e				í				64;	Length 162;	Indels	
			<u>۔</u>	te)			ta;	dae		43		. 1	₹	ر. ان	አ	Bor	-Da	•		X						×		CRC			
			date	upda			ebra	nini				<	mon	68 t	ij		ftor	er H	Ä,	7							į	7 PE	4, 0	0	
	¥		ď	6			Pert	HO					Ha	3	r L	ta	3	bat	ter	lve				Ž.	;		Z	AB.	86	. m	
	162 AA.		Last sequence update)	annotation update)			a;	H				æ}	Ä	3	ijpe	Shic		¥.	Š	inv			- 1	*. **. **.	;	NAS	men	GO; GO:0007165; P:signal transduction; NAS. SEQUENCE 162 AA; 18652 MW; 54EFD4EED3AB97FE CRC64;	Score 850; DB 4;	Mismatches	
		g	ē	OH			iat	rrh				2	Bon	×	3		片	0	ä	re	 E					:- 	đo i	FD4	9,	L SEE	
	PRT;	Created)	St.	Last a			Crar	Cate				504	Ř	H K	ບ່	ì	Grai	파다	ᄷ	i i	ion					7	dev	duct 541	800	Σ̈́	
												1081	я. :	adde	andt	Ber	÷	ري د	딛	cept	regulation of lymphocyte function.";		EMBL; AF254069; AAG29348.1;		NA.	a C	פענ	rane MW;	an a	. 0	
			16,				Chordata;	Primates;				를	ខ	ž `	Br	Я.,	re	o H	_ .:	re	ei Ei	,			189	ine.	6	11 152 1	100.08;	ive.	
	PRELIMINARY;	(TrEMBLrel.	E	(TrEMBLrel.		_						ъЖe	1110		Σ	l S	Š	Υa,	≖ ≿	ita	Scyt	60	2934	į.	nc re	ğ	d W	igna 186	25	Conservative	
	IMI	MBL	MBL	Mer		1	Oa:	ia;			Ä	<u></u>	Ä	isto]	pel	nel	Ü	Ä	ans	and	ď	20	AAG	H .:-1	 	о н 1	1.0	9. 4. 8. 4.		ë Y	
	PREL	(TřE	(Tre	(Tre	21.	Ď	taz	ther	606;		z Z	1754	ъ.	Sohr	Hei	Pres	663	hing	aush	21	f L	7-63	69;	900	34;	22	15;	65,		Cons	
	-	101	100			į	Romo Bapiens (Auman) Rukarvota: Metazoa:	Mammalia, Butheria;	NCBI_TaxID=9606;		SEQUENCE FROM N.A.	2053	lova		ŝ	:	ជ	: :	×	ıkin	e E	98:5	2540	Genew; HGNC:6005; IL21.	0026	0051	0075	100	ì	, i m i	
	4.4	01-MAR-2001	01-MAR-2001	01-JUN-2003	Interleukin	1	V a p	lia	Tax		SCE	SE	ah-1	J.	ead	in I	so.	LG TE	Σ Ή	rle	atio	9	A	Ħ :	Ö	ο Q	õ	NCE O	tch	16	
н	O9HBE4	A.	Α̈́	5	ter	1121.	kar Ikar	mma	H	크	500	Soli	iri	9890	춫	덡	idri	L YOU	aure	Inte	977	at uz	Ē,	ene	Ö	Ö	Ö	30, 30, 30, 30,	×	Jes Jes	
RESULT 09HBE4	öö	5	6	8	Ä	Ħ :	č G	iΣ	ž		S	Ξ	ă	G	щ		₹	~	Ë	=	ដ	ž	Ø	Ŏ,	შ	დ (Ø.	დ დ	Query Match	Best Local Similarity Matches 162; Conserv	
RESULT O9HBE4	n a	1	占	텀	DE I	Z 2	200	88	ŏ	Z	RР	RΧ	ð	æ	æ	æ	Z	Z	Z	RT	R.	띩	띴	ద	K K	K I	ŭ	S S	O I	u ≥;	

1 MRSSPGNMERIVICLMVIPLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF 60

ö

```
PRELIMINARY;
          NCBI_TaxID=10042;
                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          136 FLE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tambourgi D.V.;
                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q81913
Q81913;
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
Q81913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
 STARRAN
                                                                                                                                                                                                                                             ଟ
                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 ETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKREPSTNAGRROKHRLTCPSCDS 127
                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MERTILVCIAVIFIGIVAHKSSPQGPDRILIRIRHLIDIAVEQLKIYENDLDPELLSAPQDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                Parrish-Novak J., Dillon S.K., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kuijper J.L., Kramer J., Conklin D., Presnell S.R., Barry J., Shiota F., Bort S., Hambly K., Mudri S., Clegg C., Moore M., Grant F.G., Lofton-Day C., Gilbert T., Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maushansky K., Holly R.D., Foster D.;

"Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";

Nature 408:57-63(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 MERIVICIANVIFIGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPBFLPAPEDV
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peromyscus maniculatus (Deer mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.2%; Score 486; DB 11; Length 146; 63.0%; Pred. No. 2.9e-42; ive 23; Mismatches 31; Indels (
                                                                                                                         TCPSCDSYEKKPPKEFLERPKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                   TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UUN-2003 (TrEWBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Interleukin-21 (Fragment).
                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 AA
                                                                                                                                                                                                     146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YEKRTPKEFLERLKWLLOKMIHOHLS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEKKPPKEFLERFKSLLQKMIHQHLS 153
                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/c;
MEDLINE=20531754; PubMed=11081504;
                                                                                                                                                                                                                               01-MAR 2001 (TEMBLEEL 16, 01-MAR-2001 (TEMBLEEL 16, 01-OCT-2003 (TEMBLEEL 25, Interleukin 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 63.0 tes 92, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                              61
                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q80XG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                         29ES17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                  셤
                                                                         셤
                                                                                                      à
                                              ठे
```

```
94 -RIINVSIKK--LKRKPPSTNAGRROKHRLTCPSCDSYBKKPPKEFLERFKSLLOKMIHQ 150
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 PTYSYHGTPCDFGRDCIRWEYPDVPLQTLRDYTTPGNSKYYEKFILFVLDLKTGSLANNNE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FACFOXAKIKPANTGSNKTIISDLVTQLARRIPATKAEKKQQSLVKCPSCDSYEKKTPKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and expression of a functional dermonecrotic and haemolytic factor from Loxosceles laeta venom.";
Blochem. Biophys. Res. Commun. 298:638-645 (2002).
ENEL; AV093600; AAM21155.1;
GO; GO:0008889; F:glycerophosphodiester phosphodiesterase act...; IEA.
GO; GO:0006071; F:glycerol metabolism; IEA.
InterPro; IPR004129; GDPD.
Fam; PP03009; GDPD; 1.
SEQUENCE 311 AA; 35451 MW; 39040BB3A21F56E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                       16 MVIFLGTLVHKSSSQGODRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSA
                                                                                                                                                                                                                                                                                                                                                                                                        76 FSCFOKAQLKSANTGNNERIINVSIKKUKRKPPSTNAGRROKHRLTCPSCDSYBKKPPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 IVICLAVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVND------LV
Schountz T., Buniger A., Davenport B., Hegg T.; "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4 cDNAB.";
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUBE-Venom gland;
MEDLINE-22206580; PubMed=12419302;
Pedrosa M.F.F., Junqueira de Azevedo I.L.M.,
Goncalves-de-Andrade R.M., van den Berg C.W., Ramos C.R.R., Ho P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sphingomyelinase-like protein.
Loxosceles laeta.
Eukaryota; Merazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
                                                                                                                                                                                                                                                                                                                    ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                              Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 85; DB 5; Length 311; 23.1%; Pred. No. 1.8; .tive 23; Mismatches 71; IndelB
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                         Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY247761; AAP04420.1; -.
                                                                                                                                                                             123 123
123 AA; 13945 MW; 8656C8EA95447E34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                              Query Match
46.1%; Score 392; DB 11;
Best Local Similarity 60.2%; Pred. No. 1.2e-32;
Matches 74; Conservative 24; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.1%
Matches 42; Conservative
```

```
SEQUENCE FROM N.A.
MEDLINE=94200956; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viral proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nurhayati E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potyvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       082933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BME1, AE016609; AA007435.1; -..
BME1, AE016609; C.membrane; IEA.
GO; GO:00016629; C.membrane; IEA.
GO; GO:0001669; F.ATP binding; CAS.
R GO; GO:000166; F.Inucleotide binding; IEA.
R GO; GO:0001669; F.Inucleotide binding; IEA.
R GO; GO:0001669; F.Inucleotide binding; IEA.
R GO; GO:0001669; F.Inucleotide binding; IEA.
R GO; GO:0001669; F.Inucleotide binding; IEA.
R InterPro; IPR001349; AAA ATPASE.
R InterPro; IPR001349; ABC transporter.
R InterPro; IPR00140; ABC transporter.
R InterPro; IPR00164; Uridine kin.
R InterPro; IPR00164; ABC membrane; I.
R InterPro; IPR00164; Lani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 PALIENNHGW------QVITQVSDGHWTPYDPSTQQLQTQPVSPNPSQR-KHKVMLL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 PEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRPPSTNAGRROKHRLTCP 123
128 VRKAGENIAKGLLKNYWNNGNNGGRAYVVLSLPDIAHY-----EFIRRFKEVLKAEGHE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 VIFLGTLVHKSSSQGQDRHMI------RMRQLIDIVDQLKNYVNDL---VPEFLPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.9%; Score 84.5; DB 16; Length 722;
Best Local Similarity 25.0%; Pred. No. 5.4;
Matches 36; Conservative 26; Mismatches 57; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong Choy H.E.;
                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC-type bacteriocin/lantibiotic exporters.
VV20484.
VD1rio vulnificus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionacee; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      722 AA; 79857 MW; B8967F3B930C0205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           582 AA
                                                                                                                                                                               722 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Complete proteome.
FORGERICE 722 AA; 79857 MW; B8967F3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCDSYEKKPPKEFLERF-KSLLQK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00988; URIDINKINASE.
Prodom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ADEQLSSKEVKFGLSWFAPSILRQ 164
                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-JUN-2003 (TrEMBLrel. 24, Trill46 protein.
                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=672;
                                        151 HL 152
                                                                 :|
182 NL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBDJS6
                                                                                                                                                                               Q8D6P4
                                                                                                                                       RESULT 5
28D6P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
  g
                                                                                ል
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                          ਨ੍ਹੇ
```

```
-----1TCP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence of Johnson grass mosaic potyvirus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnsongrass mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                    Nakamura Y., Kaneko T., Sato S., İkeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sibmitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
9.8%; Score 83.5; DB 16; Length 582;
Best Local Similarity 21.6%; Pred. No. 5.4;
Matches 21; Conservative 24; Mismatches 31; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEROPS; S30.001; -.
OC GO:0019028; C:viral capsid; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP dependent helicase activity; IEA.
GO; GO:0004197; F:systeine-type endopeptidase activity; IEA.
GO; GO:0014197; F:hydrolase activity; IEA.
GO; GO:001676; F:hydrolase activity; IEA.
GO; GO:0003676; F:hydrolase activity; IEA.
Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gough K.H.; Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 AA; 66407 MW; DF0A33E93614A92D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 KAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 SCDS-YEKKPPKEFLERFKSLLQKMIHQHLSSRTHGS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 EADSDYHQLPPETLAQQWRDILQEQMNQAIQERTHAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AP005372; BAC08688.1; -.
GO, GO:0016020; C:membrane; IEA.
InterPro; IPR066885; M3ion_channel.
Pfam, PF00924; MS_channel; 1.
Complete proteome.
SEQUENCE 582 AA; 66407 MW; DF0A3
                                                                                                                                                                                                                MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94200956; PubMed=8150599;
Gough K.H., Shukla D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intervirology 36:181-192(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z26920; CAA81549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 9:123-130(2002)
```

```
SEQUENCE
  REARING SELECTED SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 IVDOLKNYVNDLVPRFLPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 LVNALDQYEED-VKQICHYSFDAEARAFWKGFTENHTAQRREAHDHTNHEPV-MSVEEGG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Furuya N., Komano T., "Nucleotide sequence and characterization of the trbABC region of the Incll Plasmid R64: existence of the pnd gene for plasmid maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMALL NUCLEAR INCLUSION/VIRUS ATTATCHED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMALL NUCLEAR INCLUSION/PROTEASE.
LARGE NUCLEAR INCLUSION/POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 3052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 RRAAMLENAFHQGFKITCKHCFQTFDEHSDESVCERIHNALQRIBEQN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 RKPPSTNAGRROKHRLTCPSC-DSYEKKPPKFFLERFKSLLQKMIHQH 151
GO, GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0006530; P:transcription; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase C.
InterPro; IPR001650; Helicase C.
InterPro; IPR001525; Peptidase C6.
InterPro; IPR001525; Peptidase C6.
InterPro; IPR001546; Peptidase C6.
InterPro; IPR001546; Peptidase C6.
InterPro; IPR001546; Peptidase C6.
InterPro; IPR001540; Peptidase C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 83.5; DB 12; Length 30
23.1%; Pred. No. 38;
ive 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6KI.
CYTOPLASMIC INCLUSION (CI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3052 AA; 347247 MW; 08CD8831A73EBCA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coat protein, Helicase, Hydrolase.
139 699 HELPER COMPONENT (HC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             899 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COAT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEASE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                            ; IPRO02540; FOLY_FI.
; IPRO07095; RNA_POL_DS_PS.
; IPRO01205; RNA_POL_P3D.
(271; PRE007094; RNA_POL_PSVIr.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                     Pfam, PF00767; Poty_coat; 1.
Pfam; PF01577; Poty_P1; 1.
Pfam; PF00680; RNA_dep_RNA_pol; 1.
SMRTNS; PR00966; NTAPOTYPTASE.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      within the transfer region.";
J. Bacteriol. 178:1491-1497(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-drd-11; PLASMID-R64;
MEDLINE-96198148; PubMed-8626273;
                                                                                                                                                                                                                                                                                                 Pfam, Pro0863; Peptidase C4; 1.
Pfam, Pro0851; Peptidase C6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ol-NOV-1996 (TrEMBLrel. 01
01-NOV-1996 (TrEMBLrel. 01
01-UNV-2003 (TrEMBLrel. 24
NikB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 23.19
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                            Pfam, PF00271; helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2749
3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid R64.
                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                              nterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             052336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
STEAIN=drd-11; PLASMID=R64; MEDLINE=91177811; PubMed=1848841; Furuya N., Nisioka T., Komano T.; "Nucleotide sequence and functions of the oriT operon in IncIl plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87146423; PubMed=3029698; Komano T., Kubo A., Nisioka T., Komano T., Kubo A., Nisioka T., Shufflon: multi-inversion of four contiguous DNA segments of plasmid R64 creates seven different open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIM=drd-II; PLASMID=R64;
STRAIM=drd-II; PLASMID=R64;
WBDLINB=99268996; PubMed=9603870;
Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K., Ogawa T., Komano T.;
Purification and Characterization of thin pili of IncII plasmids ColIb-P9 and R64: formation of PilV-specific cell aggregates by type IV pili.";
IV pili.";
Bacteriol. 180:2842-2848(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=drd-11; PLASMID=R64;
MEDLINE=94132044; PubMed=8300611;
MEDLINE=94132044; PubMed=8300611;
Pansegrau W., Schroder W., Lanka E.;
"Concerted action of three distinct domains in the DNA cleaving-
ioining reaction catalyzed by relaxase (TraI) of conjugative plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-drd-11, PLASMID-R64;
BILLINE=98053841; PubMed=9393692;
FULLVA N., Komano T.;
"Mutational analysis of the R64 oriT region: requirement for precise location of the Nikk-binding sequence.";
J. Bacteriol. 179:7291-7297(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Furuya N., Komano T.; "Determination of the nick site at oriT of IncIl plamid R64: global similarity of oriT structures of IncIl and IncP plasmids."; J. Bacteriol. 173:6612-6617(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sampei G., Komano T., Sasaki T., Tachibana K., Furuya N., Saito Y.,
Suzuki T., Mizobuchi K.;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-drd-ll; PLASMID=R64;
Kromano T., Narahara K., Yoshida T., Furuya N.;
The transfer region of Incil plasmid R64: similarities between R64
tra genes and Legionella icm/dot genes.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-drd-11; PLASMID=R64;
MEDILINE-94285211; PLASMID=R64;
Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G.,
Haas D., Helinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
"Complete nucleotide sequence of Birmingham IncP-alpha plasmids:
compilation and comparative analysis";
J. Mol. Biol. 239:623-663(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Organization and diversification of plasmid genomes: complete mucleotide sequence of R64 genome."; submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Biol. Chem. 269:2782-2789(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-drd-11; PLASMID=R64;
MEDLINE-92011438; PubMed=1917882;
Furuya N., Komano T.;
                                                                                                                                                                                      Bacteriol. 173:2231-2237(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASMID=R64;
```

Nucleic Acids Res. 15:1165-1172(1987).

```
SSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAF---SCPQKAQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Surface exclusion gene of IncI1 plasmid R64: nucleotide sequence and analysis of deletion mutants."; Plasmid 32:80-84(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89127142; PubMed=3065610;
Kubo A., Kusukawa A., Komano T.;
"Nucleotide sequence of the rci gene encoding shufflon-specific DNA
recombinase in the IncII plasmid R64: homology to the site-specific
recombinases of integrase family.";
Mol. Gen. Genet. 213:30-35 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim S.R., Funayama N., Komano T.; "Nucleotide sequence and characterization of the traABCD region of Incll plasmid R64.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Narahara K., Rahman E., Furuya N., Komano T.;
"Requirement of a limited segment of the sog gene for plasmid R64
                                                                                                                                                                                                                                                                        MEDLINE-88314948; PubMed=3045094; Komano T., Toyoshima A., Morita K., Nisioka T.; Toyoshima A., Morita K., Nisioka T.; "Cloning and nucleotide sequence of the oriT region of the Incli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim S.R., Komano T.;
"The plasmid R64 thin pilus identified as a type IV pilus.";
J. Bacteriol. 179:3594-3603(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.8%; Score 83; DB 2; Length 899; Best Local Similarity 22.5%; Pred. No. 10; Matches 34; Conservative 22; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                899 AA; 104010 MW; C062A360B275C337 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97428559; PubMed=9281491;
                                                                                                                                                                                                                                                                                                                                                       plasmid R64.";
J. Bacteriol. 170:4385-4387(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÆDLINE=93352408; PubMed=8349545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 175:5035-5042(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97315231; PubMed=9171405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95083745; PubMed=7991676; Furuya N., Komano T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asmid 38:1-11(1997)
SEQUENCE FROM N.A.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASMID=R64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LASMID=R64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "LASMID=R64
                                                                                                                                                                                                                                                     PLASMID=R64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

38

셤

```
84 LKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL---TCP-----SCDSYEKKPPK 134
                             ----ARQAHYAKDDTDPVFHYILSWQSHESPRPE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 LKSANTGNNERIINVSIKKIKRPPSTNAGRROKHRI---TCP----SCDSYEKKPPK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 SIETAAADMEYI-------ARQAHYAKDDIDPVFHYILSWQSHESPRPE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 SSSQAEQPHRSRFSRLVDYATRLRN-----BSFVALVDVMKDGCEWVNFYGVTCFHNCT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 SSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPRFLPAPEDVETNCEWSAF---SCFQKAQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Gaps
                                                                                                                                                                                                                                                                                                                        Plasmid Collb-P9.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Chen Z., Wen Y.; To the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016746; AA004261.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sampel G., Mizobuchi K.; not granting genomes: complete "Organization and diversification of plasmid genomes: complete nucleotide sequence of the Collb-P9 genome."; submitted (DEC-1998) to the EMBL/GenBank/DDDJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 9.8%; Score 83; DB 2; Length 899; Local Similarity 22.5%; Pred. No. 10; es 34; Conservative 22; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   899 AA; 103977 MW; E7DB0164C54914E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP-dependent nuclease subunit A.
                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                 135 EPLERFKSLLOKM---IHQHLSSRTHGSEDS 162
                                                                                     134 QIYDSVRHTLKSLGLADHQYVSA-VHTDTDN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 EFLERFKSLLOKM---IHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 QIYDSVRHTLKSLGLADHQYVSA-VHTDTDN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB021078; BAA75140.1; -... GO:0046821; C:extrachromosomal DNA; IEA. InterPro; IPR005094; Relaxase. Pfam; PF03432; Relaxase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1224 AA
                                                                                                                                                                                                                         Created)
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                    PRELIMINARY;
                                92 SLETAAADMEYI
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                         Shigella sonnei
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=624;
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=P9;
                                                                                                                                                                                                                                                                          Relaxase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                    Q9R2J7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSCPT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                     RESULT 9
                                                                                                                                                                        Q9R2J7
                                                                                                                                                                                                       셤
                                                                 ઠે
                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
```

```
01-0CT-2002
01-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBGFF4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE STANDARD BEAUTION OF STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STAND
       SHARRARRARRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEALNEEREROLD N. S. CEDINEERE S. E., HOLF R. A., Evans C. A., Gocayme J. D., Adams M. D., Celniker S. E., Holf R. A., Evans C. A., Gocayme J. D., Adams M. D., Celniker S. E., Holf R. A., Evans C. A., Gocayme J. D., R. Adams M. D., Celniker S. E., Holf R. A., Hoskins R. A., Galle R. F., George R. A., Lewis S. E., Richards S., Ashburner M., Henderson S. N., Stutton G. G., Wortenan J. R., Yandell M. D., Zhang G., Chen L. X. A. Brandon R. C., Rogers Y. -H. C., Jalazej K. G., Champe M., Pfeiffer B. D., R. Brandon R. C., Baxter E. G., Helt G., Nelson C. R., Miklos Gl. G., Abril J. F., Agbayani A., An H. -J., Andrews-Pfannkoch C., Baldwin D., R. Ballew R. M., Basu A., Barman B. P., Bhandari D., Bolshin D., R. Beeson K. Y. Benos P. V., Berman B. P., Bhandari D., Bolshin D., R. Burtis R. C., Busam D. A., Burler H., Cadieu E., Center A., Chandra I., Burtis R. C., Busam D. A., Buller H., Cadieu E., Center R., Chandra I., R. Aburtis R. C., Busam D. A., Buller H., Cadieu E., Davengort L. B., Davies P., Abartis N., Cavley S., Domnes M., Dugan-Rocha S., Dunkov B. C., Ferraz C., Ferraz S., Perrisca S., Ferrisca                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        963 NEIRTIEELKAINTGNEDVKIKIHQQLSYDYPRVNTWKPSKQSVSELKRQLETEESNTN 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 FSCFQKAQLKSANTGNNERIINV-----SIKKLKR----KPPSTN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIFLGTLV-HKSSSOGODRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1023 YDRVRQYRI---GVASYER--PK-FLTQTKKRKANEIGTLMHTVMQHLPPR 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AGRROKHRLTCPSCDSYEKKPPKEFLERFK-----SLLOKMIHQHLSSR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                               DB 16; Length 1224;
GO, GO:0005524; F:ATP binding; IEA.
GO; GO:0004003; F:ATP dependent DNA helicase activity; IEA.
GO; GO:000467; F:DNA binding; IEA.
GO; GO:0006281; P:DNA binding; IEA.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; I.
Complete proteome.
SEQUENCE 1224 AA; 143015 NW; 4B204F41AlaDPGAI CRC64;
                                                                                                                                                                                                                                                                                                                                           ; Score 83; DB 16; Length 12; Pred. No. 14; 22; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                               9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                      45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG15745 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VYE8
Q9VYE8;
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A PART A 
               S K R R R R R S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
Subjudice From Annual B., Rasool T.J.;
Submitted (FBE-2003) to the EMBL/GenBank/DDBJ databases.

- I- FUNCTION: CYTOXINE THAT STIMULATES THE PROLIFERATION OF T.
- I-TWH-HOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15

- ILTMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15

- INTERPOSATES STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15

- INTERPOSATES STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY IL-15

- INTERPOSATES STIMULATION BY INTERPOSATE STIMULATION BY INTERPOSATE STIMULATION BY INTERPOSATE STIMULATION BY INTERPOSATE STIMULATION BY INTERPOSATE STIMULATION BY INTERPOSATE STIMULATION BY INTERPOSATE STIMULATION BY INTERPOSATE STIMULATION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 DIGYPCEVASISELALRKAQLKAQFFGNQVG----GLARDSETSSTTRITRTTNYRSAYP 175
          Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang D.-Y., Wassarman D.A., Wahistock G.M., Welsenbach J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Glibbs R.A., Myers E.W., Rubin G.W., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
Flysmes: Falous A.F. Falous G. M. F. Flysmes: Falous A.F. Flysmes. Falous A.F. Flysmes. Falous A.F. Flysmes. Falous A.F. Flysmes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 DVETNCEWSAFS--CFOKAQLKSANTGNNERIINVSIKKLKRPPSTNAGRRQKHRLTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
, Sun E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anas platyrhynchos (Domestic duck).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Anseriformes, Anatidae, Anas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou J.Y., Wang J.Y., Chen J.G., Cheng L.Q., Zheng X.J., Gong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of Shaoxing layer duck (China) interleukin-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmohl K., Schultz U., "Chmohl K., Schultz U., "Cloning and characterization of duck interleukin-2."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-2.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 AA; 60620 MW; 31FA41FA4AEF427F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Interleukin-2 precursor (Interleukin-15) (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 SCKTERGKPVQQLIDQFQAMIVQQQQQQQLSN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SCDSYEKKPPKEFLERFKSLL-QKMIHQHLSS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Score 81.5; DE
26.1%; Pred. No. 8.3;
ative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
INTERLEUKIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003443; Interleukin_15.
Pfam; PF02372; IL15; 1.
Cytokine; Signal.
1 21 POTENTI/
CHAIN 22 140 INTERLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 22,
(TrEMBLrel. 22,
(TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Spleen;
```

g

දු

ਨੇ

à

```
Amanatides P.G., Scherer S.E., Lip P.M., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Lip P.M., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Button G.G., Wortman J.R., Zhadell M.D., Zhang Q., Chen L.X.,
Button G.G., Wortman J.R., Sandell M.D., Zhang Q., Chen L.X.,
R. Brandon R.C., Rakter S.G., Helt G., Champen M., Piefeifer B.D.,
R. Ballew R.M., Baste A. An H.-J., Andrews Feanatoch C., Baldwin D.,
R. Ballew R.M., Basto A., An H.-J., Andrews Feanatoch C., Baldwin D.,
R. Beson K.Y., Bence P.V., Bernan B.P., Bhandari D., Belshakov S.,
R. Borkova D., Botchan M.R., Bouck J., Browner Feanatoch C., Baldwin D.,
R. Burtis K.C., Busam D.A., Bulke T., Cadieu E., Center A., Chandra I.,
R. Borkova D., Botchan M.R., Bouck J., Brottler P.,
R. Borkova D., Botchan M.R., Bouck J., Brottler P.,
R. Durbin K.J., Evangelista C.C., Ferraz C., Ferrise P.,
R. Durbin K.J., Evangelista C.C., Ferraz C., Ferrise S., Dunkov B.C., Dunn P.,
R. Borkova D., Boton R., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Hortin N.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R. Hortin M., Allush F., Karpen G.H., Ke Z., Kennison J.R., Retenmin B.S., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
I.Lu X., Mattei B., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
I.Lu X., Mattei B., Norlinchoh T.C., Morris J., Moshrefi A.,
Rulson D.R., Nelson K.A., Li J., Warny D.M., Nelson D.L.,
R. Anner K., Remington K.A., Minskern D.R., Pacleb J.M.,
R. Anner E., Spradling A.C., Stapleton M., Skrong K., Wilson K., Martei E., Spradling A.C., Stapleton M., Skrong K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Wilson K., Shen H.,
R. Spier E., Spradling A.C., Stapleton M., Strong K., Strong K., Strong K., Wilson G., Wilson B., Wilson B., Wilson B., Wilson B., Wilson B., Wilson B., Wilson B., Wilson B., Wilson B
                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pteryge
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metal-binding; Zinc, Zīnc finger. —
SEQUENCE 385 AA; 43943 MW; 24DOEAE4CSFD5DA6 CRC64;
                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMARI; SRUGISS; SENGERINGER C2H2 1; 6.
PROSITE; PS501028; ZINC_FINGER_C2H2_2; 6.
                                                                   385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase, FBgn0028895, BG:DS02740.8.
InterPro, IPR007087, Znf C2H2.
Pfam; PF00096; zf-C2H2; 6
                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003650; AAF53516.1; -
HSSP; P08046; 1A1I.
                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2H2; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                   BG: DS02740.8 protein.
BG: DS02740.8 OR CG17328.
                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                       Q9VJL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 VNDLVPBFLPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNA 112
                                                                                                                                                                                                                                                                                                                                                                       71 CEWSAFSCFOK-----AQLKSANTGNNERI-----INVSIKKLKRK-PPSTNAGRROKH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CSWQTLOCYLKEIVTLEEEIEDEDEIEDEKVSSVRNIKMNLQKLMDLIPPGTG----- 113
                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                       6 IPSCLSVLMLMTTAYGAPLSEKDN---TLKTLIKDLENLGTSMNGIDLE-LYTPNDTK-E 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 INBIKPTILKCDKNKDRQ-----YSIDBIVQLLKKNBKNPERLAVLFKSLAKKLDESIC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glocckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgar L., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A., "Sequence and analysis of chromosome 2 of Dictyostellum discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                       11 IVICLAVIFLGTLVHKSSSQGODRHMIRARQLIDIVDQLKNYVNDLVPEFLPAPEDVETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Gaps
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.5%; Score 81; DB 5; Length 163; Best Local Similarity 25.5%; Pred. No. 2.2; Matches 26; Conservative 17; Mismatches 51; Indels
                                                                   Query Match 9.5%; Score 81; DB 13; Length 14: Best Local Similarity 22.0%; Pred. No. 1.8; Matches 33; Conservative 29; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishio K., Yokoyama M., Maeda M.;
"Novel calcium binding proteins in Dictyostelium.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB070450; BAB63908.1; -.
EMBL; AC117176; AA052155.1; -.
GO; GO:0005509; F:calcium ion binding; IRA.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 GRROKHRLTCPSCDSYEKKPP---KEFLERFKSLLOKMIHQH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNDIDDREISKNCDKFQDKPEIDIESFLLRFDKNNDKMISHH 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4ypothetical protein.
SEQUENCE 163 AA; 18924 MW; AF0BCF63C7FFCF8F CRC64;
140 AA; 15965 MW; 0154D832F3039410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Calcium binding protein CBP9 (Hypothetical protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 RLTCPSCDSYEKKPPKEFLERFKSLLQKMI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 --- CNICEANANNPP-EFROELTNFLRSML 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22092622; PubMed=12097910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00018; EF_HAND; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=AX4;
Baumgart C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KAX4;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
```

Q966R0

```
12 VICLMVIF-LGTLVH-KSSSQGQDRHMIRWRQLIDIVDQLKNYVNDLVPEFLPAPEDVET 69
Match 9.5%; Score 81; DB 5; Length 385; Local Similarity 22.2%; Pred. No. 6; Local Similarity 22; Mismatches 44; Indels les
```

셤 ð

à

24 VIONCITALIANA PREPROBERENDO "LARLAQUIGILESSAR"						•		
15 NCENCITALGVARHENDECENSDIRLAQUIGIESGR	_				٠.			
O O O O O O O O O O O O O O O O O O O	24 VICNNCIYRLGVAFHFKQECENSDLRLRQYLGILBSWRQDAAT	70 NCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYE 12 :	130 KKPPKEPLERFKSLLQKMIH	100 RKPPEBHKKRGPKPVPKMPHTCYBCHKSFKCIAQLTQHIRTHTGB	NK60 O9NK60 PRELIMINARY, PRT; 414 AA. O9NK60; C1-C0T-2000 (TERMELrel. 15, Last sequence update) 01-C0T-2000 (TERMELrel. 25, Last annotation update) 01-C0T-2003 (TERMELrel. 25	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE STRAINE-BERKELEY; MEDLINE-99403001; PubMed=10471707; MEDLINE-99403001; PubMed=10471707; Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., D Ashburner M., Misraell G., Har Bonyle C., Galle R., George R., Harris N., Harrisall G., Martin C., Mc Houston K., Hoskins R., Johnson G., Martin C., Mc Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., "An exploration of the sequence of a 2.9-Mb region of the Drosophila melanogaster: the Adh region.";	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-Berkeley; Celniker S.E. Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Celniker S.E. Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A., Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B. Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi Nixon K., Pacleb J.M., Park S., Pfelifer B., Poon L., Sequeira A. Sethi H., Snir E., Suriskas R.R., Wan K.H., Weinburg T., Zhang R. Zieran L.L., Rubin G.M.; Park S., Man K.H., Weinburg T., Zhang R. EMBL, AR003415, AR44998.1;	Query Match Best Local Similarity 22.2%; Pred. No. 6.5; Matches 37; Conservative 22; Mismatches 44; Indels 64; Gaps 12 VICLMVIP-LGTLVH-KSSSQGORHMIRMRQLIDIVDOLKNYVNDLVPEFLPAPEDVET 69

: YQ 128		
: RRSR	OHLSSRTHGSE 160	129 RKPPEEHKKRGPKPVPKMPHTCYECHKSFKCIAQLTQHIRTHTGE 173
: KVSK	-	KCIA
:: :	;	HKSF
96 NTDFVEKPLLPQRDSDEBEPVDAKVSK	130 KKPPKEFLERFKSLLQKMIH	KMPHTCYEC
-FVEXPLE	BRFKSLLQ	CKRGPKPVP
; CTN	KKPPKEFI	RKPPEEHI
9 9	130	129
ą	È	අු

Search completed: March 3, 2004, 12:38:09 Job time : 28.4706 secs

```
TYPE: PRT
CRGANISM: Homo sapiens
US-09-522-217-2
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-522-217-2
Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                           3, 2004, 12:33:10; Search time 11.3824 Seconds (without alignments) 734.770 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                 US-09-825-561A-10
850
1 MRSSPGNWERIVICLMVIFL......LLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-09-522-217-85
S-09-923-246-85
S-09-923-246-85
S-09-923-246-56
S-09-923-246-56
S-10-295-723-56
S-09-923-246-89
S-10-295-723-89
S-10-295-723-89
S-10-295-723-89
S-10-295-723-89
S-10-295-723-72
S-09-923-247-72
S-09-923-246-73
S-09-923-246-73
                                                                                                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                             March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             850
850
850
695.5
695.5
695.5
486
486
486
486
394
394
394
394
212
212
212
212
217
617
617
617
                                                                                                                                                                                                                      score:
                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                   Fitle:
Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on
```

```
LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                              Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
               Sequence
                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                       Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 850; DB 4; Length 1
Best Local Similarity 100.0%; Pred. No. 1e-86;
Matches 162; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCPSCDSYEKKPPKEPLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/0952217

Sequence 2, Application US/0952217

Patent No. 6307024

GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Poster, Donald C.
APPLICANT: Gores, Jane A.
APPLICANT: Gores, Jane A.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Hollon, Stacey R.
APPLICANT: Hammond, Angela K.:
APPLICANT: Dillon, Stacey R.
APPLICANT: Barmond, Angela K.:
APPLICANT: Barmond, Angela K.:
APPLICANT: Now Stacey R.
APPLICANT: Barmond, Angela K.:
APPLICANT: Now Now C. CYTOKINE ZALPHAII LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US 60/123,547
EARLIER PILING DATE: 1999-03-09

RARLIER PILING DATE: 1999-03-01

RARLIER FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: PastEEQ for Windows Version 3.0

SEQ ID NO 2.
                                                  US-08-393-305-2
US-08-238-733-2
US-08-258-733-2
US-08-725-969-2
US-08-725-969-2
US-08-194-947-6
US-09-189-193-2
US-09-223-217-113
US-09-223-246-113
US-09-223-246-113
US-10-295-723-113
PCT-US96-06423-2
                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
```

```
; ORGANISM: Homo sapiens
US-10-295-723-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-522-217-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                             ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRSSPGNMERIVICLMVIFLGTLVHKSSSGGDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: BARLIER FILING DATE: 2000-03-09
PRIOR PILING DATE: BARLIER PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/123,904
PRIOR PILING DATE: BARLIER PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/142,013
PRIOR PILING DATE: BARLIER PILING DATE: 1999-07-01
NUMBER OF SEC ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 850; DB 4; Length 162
Best Local Similarity 100.0%; Pred. No. 1e-86;
Matches 162; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
            APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REPERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10295723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: No. 6686178ak, Julia E
APPLICANT: No. 6605272ak, Julia E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWAKE.
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-923-246-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ⋧
```

```
83 OLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLICPSCDSYEKKPPKEFLERFKS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LPAPEDVETNCEWSARSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 LVPRGS---QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LPAPEDVETNCEWSAPSCPOKAQLKSANTGNNERIINVSIKKLKRPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRSSPGNWERIVICLMVIFLGTLVHKSSSQGOBHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LVHKSSSQGDDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide US-09-522-217-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 695.5; DB 4; Length 519;
Pred. No. 6.7e-69;
1; Mismatches 2; Indels 3
                                                                                                                                                                                                                                                                                                                                           Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCPSCDSYEKKPPKEFLERFKSLLOKMIHOHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Gener, Donald C.
APPLICANT: Gross, Jane A.
APPLICANT: Obniston, Janet V.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Branch Angela K.
ITILE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND FILE RPERENCE: 99-16
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-01
EARLIER FILING DATE: 1999-03-01
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 85: LENGTH: 519
                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 850; DB 4; Best Local Similarity 100.0%; Pred. No. 1e-86; Matches 162; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PRESEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 85, Application US/09522217
Patent No. 6307024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.7%;
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 LVPRGS---QDRHMIRAMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 QLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 OLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS 499
440 QLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLICPSCDSYEKKPPKEFLERFKS 499
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FOREER, Donald C.
APPLICANT: Holly Richard D.
APPLICANT: Holly Richard D.
APPLICANT: Hollon, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Johnston, Janet V.
APPLICANT: Dillon, Stacey W.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER PILING DATE: 1999-03-09
PRIOR PILING DATE: EARLIER PILING DATE: 1999-03-11
PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR PILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER: OF SEC ID NOS: 115
SOFTAMER PERSENCE: PARLIER FILING DATE: 1999-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 LVHKSSSQGQDRHMIRWRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide
US-09-923-246-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%; Score 695.5; DB 4; Length 519; 95.7%; Pred. No. 6.7e-69; tive 1; Mismatches 2; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLOKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 LLOKMIHOHLSSRIHGSEDS 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10295723
                                                                             143 LLOKMIHOHLSSRINGSEDS 162
                                                                                                                                                                                                                                                           Application US/09923246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Presnell, Scott R.
                                                                                                                               500 LLOMINOHLSSRTHGSEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.7
Matches 134; Conservative
                                                                                                                                                                                                                                     -09-923-246-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 85
LENGTH: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              심
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                              გ
                                                                             ⋩
```

```
383 LVPRGS---QDRHMIRNRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 QLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDSYBKKPPKEFLBRFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 LVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCPQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 QLKSANTGNNERIINVSIKKLKRPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
7. OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide
US-10-295-723-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vacuation 10 (19522217)

Sequence 56, Application US/0952217

Patent No. 6307024

GENERALINFORMATION:
APPLICANT: Presnell, Scott R. APPLICANT: Poster, Cindy A. APPLICANT: Poster, Cindy A. APPLICANT: Constol, C. APPLICANT: Constol, C. APPLICANT: Gones, Jane A. APPLICANT: Gones, Jane A. APPLICANT: Holly, Richard D. APPLICANT: Obnical C. APPLICANT: Mison, Andrew J. APPLICANT: Mison, Andrew J. APPLICANT: Mison, Andrew J. APPLICANT: Nalson, Nalson, CURRENT APPLICATION, NUMBER: US 60/123,547

EARLIER, APPLICATION, NUMBER: US 60/123,547

EARLIER, PILING DATE: 1999-03-11

EARLIER PILING DATE: 1999-03-11

EARLIER PILING DATE: 1999-03-11

EARLIER PILING DATE: 1999-03-11

EARLIER PILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115-004

SEQ ID NOS: 115-004

SEQ ID NOS: 115-004

SEQ ID NOS: 115-004

SEQ ID NOS: 115-004
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

81.84; Score 6955; DB 4
Best Local Similarity 95.74; Pred. No. 6.7e-69;
Matches 134; Conservative 11; Mismatches 2
          TITLE OF INVENTION: NOVEL.

URLE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/10/295,723

CURRENT FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR FILING DATE: 1999-09

PRIOR FILING DATE: 1999-00-10

PRIOR FILING DATE: 1999-00-11

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

NUMBER: OF SEQ ID NOS: 115

SEQ:THARE: PRECEST FOR WINDOWS VERSION 3.0

SEQ:ID NO 85

LENGTH: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 LLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 LLOKMIHOHLSSRTHGSEDS 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
```

g à g ò

```
68 BINCEWSAFSCFOKAQLKSANTGNNERLINVSIKKLKRPPSTNAGRROKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 MERIVICIANVIFIGTLYHKSSSQGQDRHMIRARQLIDIVDQLKNYVNDLVPEFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 1999-03-09
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: No. 6307024ak, Julia
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Foster, bonald C. APPLICANT: Holly, Richard D. APPLICANT: Gross, Jane A. APPLICANT: Johnston, Janet V. APPLICANT: Nelson, Andrew J. APPLICANT: Dillon, Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.0%
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: mus musculus US-10-295-723-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 ETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 ETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRPPSTNAGRROKHRLTCPSCDS 127
                                                                                                                            8 MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 MERIVICIMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/522,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                ;
0
     Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Indels
                                                31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: No. 0002/22K, Julia E.
APPLICANT: Specher, Cindy A.
APPLICANT: Specher, Cindy A.
APPLICANT: Specher, Conald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gones, Jane A.
APPLICANT: Johnston, Jane A.
APPLICANT: Nelson, Andrew J.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND
FILE RFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.2%; Score 486; DB 4; 63.0%; Pred. No. 2.5e-46; tive 23; Mismatches 31.
57.2%; Score 486; DB 4;
63.0%; Pred. No. 2.5e-46;
iive 23; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                        128 YEKKPPKEFLERFKSLLOKMIHOHLS 153
                                                                                                                                                                                                                                                                                                                                   121 YEKRTPKEFLERLKWLLOKMIHOHLS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09923246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Conservative
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 92; Conservat
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
     Query Match
Best Local S
Matches 92
```

9

Gaps

.; 0

```
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
ERALIER APPLICATION NUMBER: US 60/123,547
ERALIER APPLICATION NUMBER: US 60/123,904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER PELING NUMBER: US 60/123,904
EARLIER PILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
                                                                                128 YEKKPPKEFLERFKSLLQKMIHQHLS 153
                                                                                                                                      121 YEKRTPKEPLERLKWLLOKWIHOHLS 146
```

Application US/10295723

Sequence 56, Applica Patent No. 6686178 GENERAL INFORMATION: US-10-295-723-56

ò

В ઠે

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 DRILIRLRHIIDIVEQLKIYENDLDPELLSAPQDVKGHCEHAAFACFOKAKLKPSNPGNN 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449
                                                                                                                                                                                                                                                                                                                                                                                         93 ERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHL 152
                                                                                                                                                                                                                                                                                                                                                                                                                 33 DRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEMSAFSCFOKAQLKSANTGNN
                                                                                                                                                                                                                                                                                                                                 390 DRILIRLRHLIDIVEQLKIYENDLDPELLSAPQDVKGHCEHAAFACFQKAKLKPSNPGNN
                                                                                                                                                                                                                                                                                               33 DRHMIRMROLIDIVDOLKNYVNDLVPRFLPAPEDVETNCEWSAFSCFOKAQLKSANTGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PELICATION NUMBER: ERRIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: ERALIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER PEPLICATION NUMBER: US 60/123,904
PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER PILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: MBP-mouse zalphall Ligand fusion polypeptide US-09-923-246-89
                                                                                                                                   ; OTHER INFORMATION: MBP-mouse zalphall Ligand fusion polypeptide
US-09-522-217-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 46.4%; Score 394; DB 4; Length 510; Best Local Similarity 62.0%; Pred. No. 2e-35; Matches 75; Conservative 19; Mismatches 27; Indels
                                                                                                                                                                                                     Ouery Match
Best Local Similarity 62.0%; Pred. No. 2e-35;
Matches 75; Conservative 19; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-100 CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 89 LENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: No. 6605272ak, Julia E. APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A. APPLICANT: Foster, Donald C. APPLICANT: Holly, Richard D. APPLICANT: Gross, Jane A. APPLICANT: Johnston, Janet V. APPLICANT: Nelson, Andrew J. APPLICANT: Nelson, Andrew J. APPLICANT: Lammand Stacey R. APPLICANT: Lammand Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09923246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 $ 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 $ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 89
LENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450
                                                                                                                FEATURE:
                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                          음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                           ਨ੍ਹ
```

```
93 ERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 DRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFOKAQLKSANTGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: MBP-mouse zalphall Ligand fusion polypeptide US-10-295-723-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.4%; Score 394; DB 4; Length 510;
62.0%; Pred. No. 2e-35;
live 19; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                              APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 2002-11-15

PRIOR APPLICATION NUMBER: 09/522,217

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 1999-03-09

PRIOR PILING DATE: 1999-03-09

PRIOR PILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR APPLICATION NUMBER: US 60/123,004

PRIOR APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SEQ ID NO 89

LENGTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510
                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 72, Application US/09522217
Patent No. 6307024
Sequence 89, Application US/10295723
Patent No. 6686178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: No. 6307024ak, Julia
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                        ohnston, Janet V
                                                                                                                                             Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.0%
Matches 75; Conservative
                                                                                                                                                                                                                                             Nelson, Andrew J.
Dillon, Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foster, Donald C. Holly, Richard D. Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 S 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $ 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510
```

449

us-09-825-561a-10.rai

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Johnston, Jamer A.
APPLICANT: Ochnston, Jamer V.
APPLICANT: Dohnston, Andrew J.
APPLICANT: Dohnston, Andrew J.
APPLICANT: Dillon, Stacey R.
FILE REFERENCE: S9-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT APPLICATION NUMBER: BALLIER APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PSELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.9%; Score 212; DB 4; Length 40; Best Local Similarity 100.0%; Pred. No. 1.3e-16; Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ODRHMIRMRÓLIDIVDÓLKNÝVNDLVPEFLPAPEDVETNC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.9%; Score 212; DB 4; I 100.0%; Pred. No. 1.3e-16; tive 0; Mismatches 0;
Hammond, Angela K. .
WENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
                                                                           CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT APPLICATION NUMBER: US 60/123,547
EARLIER PILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PARKSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: HuzalphallL-1 peptide US-09-923-246-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; CIHER INFORMATION: HuzalphallL-1 peptide
US-09-522-217-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09923246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 72
LENGIH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9%; Score 212; DB 4; Length 40;
100.0%; Pred. No. 1.3e-16;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND FILE REFERENCE: 99-100 PARTICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: HuzalphallL-1 peptide
US-10-295-723-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: March 3, 2004, 12:39:56 Job time : 12.3824 secs
Application US/10295723
                                                                                                                                                                                                    Johnston, Janet V.
Nelson, Andrew J.
Dillon, Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                        Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.v
...-hes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

March 3, 2004, 12:38:15 ; Search time Run on:

US-09-825-561A-10

850 1 MRSSPGNMERIVICLMVIFL.....LLQXMIHQHLSSRTHGSEDS 162 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

809742 segs, 211153259 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					١.	3		,							į	
	Description	Sequence 2, Appli	Sequence 10, Appl	Sequence 19, Appl	Sequence 19, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 85, Appl	Sequence 85, Appl	Sequence 56, Appl	Sequence 47, Appl	Sequence 56, Appl	Sequence 4, Appli
SUMMAKIES	ŒΙ	US-09-923-246-2	US-09-825-561A-10	US-09-972-218A-19	US-10-264-634-19	US-10-295-723-2	US-10-282-622-2	US-10-456-780-2	US-10-282-622-6	US-10-282-622-4	US-09-923-246-85	US-10-295-723-85	US-09-923-246-56	US-09-825-561A-47	US-10-295-723-56	US-10-456-780-4
	DB	6	6	10	14	14	14	15	14	14	σ	14	σ	σ	14	15
	% Query Match Length DB	162	162	162	162	162	162	162	162	147	519	519	146	146	146	146
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.8	89.2	81.8	81.8	57.2	57.2	57.2	57.2
	Score	850	850	850	850	850	850	850	831	758	695.5	695.5	486	486	486	486
	Result No.	-	8	m	4	ī	9	7	8	δ	10	11	12	13	14	15

Sequence 89, Appl	Sequence 89, Appl	Sequence 72, Appl	Sequence 72, Appl	Sequence 73, Appl	Sequence 73, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 4, Appli	4	Sequence 113, App	Ge 6	Ξ	o,	0	6	Sequence 3, Appli	(Z)	7	о О	6, Ap	Sequence 48, Appl	49,	41	Sequence 7, Appli	e 24,	39, A	639	Sequence 939, App	
9 US-09-923-246-89	14 US-10-295-723-89	9 US-09-923-246-72	14 US-10-295-723-72	9 US-09-923-246-73	14 US-10-295-723-73	-10	14 US-10-400-708-20	₩.	a.	9 US-09-855-313A-4	ட	5-2	14 US-10-295-723-113	-282-	-45	-275-	14 US-10-385-072-3	9 US-09-953-323A-2	9 US-09-855-313A-2	14 US-10-245-243-8	9 US-09-899-980A-6	14 US-10-004-633-48	14 US-10-004-633-49	14 US-10-004-633-41	9 US-09-899-980A-7	14 US-10-011-548-24	14 US-10-004-633-39	14 US-10-101-464A-639	14 US-10-101-464A-939	
394 46.4 510	394 46.4 510	212 24.9 40	212 24.9 40	176 20.7 32	176 20.7 32	99.5 11.7 114	99.5 11.7 114	9.5 11.7 1	99.5 11:7 162	99.5 11.7 162	99.5 11.7 162	99.5 11.7 162	99.5 11.7 162	99.5 11.7 162	99.5 11.7 162	99.5 11.7 162	94.5 11.1 122	4.5 11.1 1	94.5 11:1 .162°	94.5 11:15 162	91.5 10.8 337	91.5 10.8 337	91.5 10.8 - 337	91.5 10.8 342	91.5 10.8 567	1.5 10.8	8	77 9.1 139	76 8.9 400	(2) 「大きない」では、「おいかい」という。
16	17	18	19	ू े	21	्र 22	23	- HP24	25	. 56	27	. 28	- 60 20	30	31	32	: 333° :	3400	ે3ટ	36	∴37	38	36	40	41	42	43	44	.45	

GARRAL INCRMATION:

APPLICANT: No. US201212446Alak, Julia E.

APPLICANT: Presnell; Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Gross, Jane A.

APPLICANT: Gross, Jane A.

APPLICANT: Melson, Andrew J.

APPLICANT: Melson, Andrew J.

APPLICANT: Hammond, Angla X.

APPLICANT: Hammond, Angla X.

APPLICANT: Hammond, Angla X.

APPLICANT: Hammond, Angla X.

APPLICANT: Hammond, Angla X.

PRICE INVENTION: NUMBER: US/09/923,246

CURRENT FILING DATE: 2004-03

PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR PILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR PILING DATE: EARLIER FILING DATE: 1999-07-01

PRIOR PILING DATE: EARLIER FILING DATE: 1999-07-01

WUMBER OF SEQ. ID NOS: 115

SEQ. ID NO 2

ILENGTH: 162 Sequence 2, Application US/09923246 Patent No. US20020128446Al

; ORGANISM: Homo sapiens US-09-923-246-2

Query Match
100.0%; Score 850; DB 9; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels

1 MRSSPGNMBRIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPBF 60

us-09-825-561a-10.rapb

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                LPAPEDVETNCEWSAFSCFÇKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitters Marthew J
Collins, Mary
Young, Deborah A.
Lowe, Leslie D.
Unger, Michelle
UNENTION: Will, Member of the Cytokine Receptor Family
NCE: 22058-552CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 162;
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Spreading

APPLICANT: Spreading

APPLICANT: West, James W.

APPLICANT: West, James W.

APPLICANT: West, James W.

APPLICANT: Freshell, Scott R.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Nelson, Andrew J.

ITILE OF INVENTION SOLUBLE ZALPHAII CYTOKINE RECEPTORS

FILE REFERENCE: 00-22

CURRENT APPLICATION NUMBER: US/09/825,561A

CURRENT APPLICATION NUMBER: US 60/194,731

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 86

SSEQ ID NO 10

LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                             121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
100.0%; Score 850; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATION NUMBER: US/09/972,218A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09972218A
No. US20030049798A1
WATION:
                                                                                                                                                                                                                                                                                                          Application US/09825561A
                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                  ò
                                                                                             ద
                                                                                                                                             ò
```

```
TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor }
TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor }
FILLE REPRENCE: G1320-79
GURRENT APPLICATION NUMBER: US/10/264 634
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: 09/560,766
FRIOR FILING DATE: 2000-05-11
FRIOR FILING DATE: 2000-05-11
FRIOR FILING DATE: 2000-05-11
FRIOR FILING DATE: 2000-05-11
FRIOR FILING DATE: 2000-05-11
FRIOR FILING DATE: 2000-10-04
FRIOR FILING DATE: 2001-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERLINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERLINVSIKKLKRKPPSTNAGRROKHRL: 120
                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                          1 MRSSPGNWERIVICLMVIFLGTLVHKSSSQGQDRHMIRWRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
100.0%; Score 850; DB 14; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e.84;
Matches 162; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 repsedsyakkpakarlakakilokminohisskihesabs 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/10264634 Publication No. US20030108549A1 GENERAL INFORMATION:
                                                                                                                                                                       100.0%;
                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Human
US-10:264-634-19
ORGANISM: Human
                                                       US-09-972-218A-19
```

```
; ORGANISM: Homo sapiens
US-10-282-622-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Sim
Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-456-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 850; DB 14; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF ILL ANDREW S.
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT APPLICATION NUMBER: US/10/295,723
FRIOR FILING DATE: 1000-03-09
PRIOR PILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-07-01
NUMBER OF EQ ID NOS: 115
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: West, James W.
APPLICANT: Work USZ0030134390Alak, Julia E.
APPLICANT: Wo. USZ0030134390Alak, Julia E.
TITLE OF INVENTION: ZALPHAII LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT PELICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESQ for Windows Version 4.0
                                                                                                                                                                        APPLICANT: No. US20030125524Alak, Julia
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10282622 Publication No. US20030134390A1 GENERAL INFORMATION:
                                                                                                Sequence 2, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Johnston, Janet V.
Nelson, Andrew J.
Dillon, Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-295-723-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                    61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERLINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LPAPEDVETNCEWSARSCFOKAQLKSANTGNNERLINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPBF 60
                                                                                                          1 MRSSPGNMERIVICIAVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRSSPGNMERIVICLMVIPLGTLVHKSSSQGODRHMIRMROLIDIVDQLKNYVNDLVPEF
                                                           Gaps
                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 850; DB 15; Length 162; larity 100.0%; Pred. No. 1.8e-84; Conservative 0; Mismatches 0; Indels 0
Length 162;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCPSCDSYEKKPPKEFFERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                  121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                 121 TCPSCDSYEKKPPKEFLERPKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TCPSCDSYEKKPPKEFLERFKSLLOKWIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10456780; Sequence 2, Application US/10456780; Publication No. US20040009150A1; GENERAL INFORMATION: APPLICAMT: Nelson, Andrew J. APPLICAMT: Hughes, Seeven D. APPLICAMT: Holly, Richard D. TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATION USE OF ILI-21 IN CANCER AND TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS FILE REPERENCE: 03-08 CURRENT APPLICATION NUMBER: US 60/387,127; PRIOR APPLICATION NUMBER: US 60/387,127; NUMBER OF SEQ ID NOS: 17; SOFTWARE: PARKER OF WINDOWS VERSION 4.0
Query Match 100.0%; Score 850; DB 14; Best Local Similarity 100.0%; Pred. No. 1.8e-84; Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10282622

Publication No. US20030134390A1

GRUERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: No. US20030134390A1ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTACONISTS
FILE REFERENCE: 01-37

CURRENT FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: 60/337,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
```

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                  1 MDSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRWRQLIDIVDQLKNYVNDLVPZF
                                                                                                                                                                                                                                                                                                                                      1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRWRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 758; DB 14; Length 147; Pred. No. 1.6e-74; 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                               97.8%; Score 831; DB 14; Length 162;
98.1%; Pred. No. 2.1e-82;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TCPSCDSYEKKPPKEFLERFKSLLDKWDHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. US20030134390Alak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTACONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR PLILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: zalphall ligand Q153ST/I156D US-10-282-622-4
                                                                                                                                                             FEATURE:

COTHER INFORMATION: zalphall ligand Q153D/I156D

US-10-282-622-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rcpscosyekrepkerierrksildrm 147
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.6%;
Matches 145; Conservative
                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.1;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

RESULT 10 US-09-923-246-85 US-08-923-246-85 Sequence 85, Application US/09923246 Patent No. US20020128446A1

```
PARTICIANT PRESENTAL STREETS AND A SPECIAL STREETS AND A SPECIAL STREETS AND A SPECIAL STREET STREETS AND A SPECIAL STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREE
```

```
128 YEKKPPKEFLERFKSLLOKMIHOHLS 153
                            ò
                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 QLKSANTGNNERIINVSIKKLKREPSTNAGRRQKHRLTCPSCDSYEKKPPKBFLERFKS 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ETNCEWSAFSCFOKAQLKSANTGNNERLINVSIKKLKRPPSTNAGRRQKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 QLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERPKS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INPORMATION:

APPLICANT: No. US20020128446Alak, Julia E.

APPLICANT: No. US20020128446Alak, Julia E.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Foster, Donald C.

APPLICANT: Gross, Jane A.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Jane A.

APPLICANT: Hammond, Angla K.

APPLICANT: Nelson, Andrew J.

APPLICANT: Novel CYTOKINE ZALPHAII LIGAND

FILE REPERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/923,246

CURRENT FILING DATE: 2001-08-03

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 MERIVICLAMVIFLGTLVHKSSSQGQDRHMIRARQLIDIVDQLKNYVNDLVPEFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                                                                                          23 LVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPRDVETNCEWSAFSCFQKA
                                                                                                                                                                                                                                                                                                                                                                          ä;
                                                                                                                                                                               ). ORGANISM: Artificial Sequence

FEATURE:

) OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide

US-10-295-723-85
                                                                                                                                                                                                                                                                                                              Query Match 81.8%; Score 695.5; DB 14; Length 519; Best Local Similarity 95.7%; Pred. No. 5.4e-67; Matches 134; Conservative 1; Mismatches 2; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.2%; Score 486; DB 9; Length 146; 63.0%; Pred. No. 6.6e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 56 LENGTH: 146
                      PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 519
TYPE: PRT
PRIOR APPLICATION NUMBER: US 60/142,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 56, Application US/09923246
Patent No. US20020128446A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 LLOKMIHOHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500 LLOKMIHOHLSSRTHGSEDS 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: mus musculus
US-09-923-246-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 92, Conserv
```

d

ò

ò

ਨ

ઠે 셤 셤

ò

```
68 ETNCEWSAFSCFOKAQLKSANTGNNERLINVSIKKLKRKPPSTNAGRROKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 MERIVICIANVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPRFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.2%; Score 486; DB 9; Length 146; Best Local Similarity 63.0%; Pred. No. 6.6e-45; Matches 92; Conservative 23; Mismatches 31; Indels
                                                                                                                                                                                                                               GENERAL LINEARATION:

JURISTANT: Sprecher, Cindy A.

APPLICANT: Sprecher, Cindy A.

APPLICANT: West, James W.

APPLICANT: West, James W.

APPLICANT: West, James W.

APPLICANT: Presnell, Scott R.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: Holly, Richard D.

APPLICANT: SOUUTEN SOUUTEN SOUUTEN SECEPTORS

FILE REFERENCE: 00-22

CURRENT FILING DATE: 2000-04-05

FRIOR APPLICATION NUMBER: US 60/194,731

PRIOR FILING DATE: 2000-04-05

FRIOR APPLICATION NUMBER: US 60/222,121

FRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 86

SOUTHARE: FastSEQ for Windows Version 3.0

SEQ ID NO 47

LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: No. USCO030125524Alak, Julia B. APPLICANT: No. USCO030125524Alak, Julia B. APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A. APPLICANT: Sprecher, Cindy A. APPLICANT: Holly, Richard D. APPLICANT: Holly, Richard D. APPLICANT: Holly, Andrew J. APPLICANT: Nelson, Andrew J. APPLICANT: Hammond, Angela K. APPLICANT: Hammond, Angela K. APPLICANT: Hammond, Angela K. APPLICANT: Hammond, Angela K. APPLICANT: Humbord, 2002-11-15
FILLS REFERENCE: 99-16
FILLS REPERENCE: 90-16
FILLS REPERENCE: 2001-15
FRICK APPLICATION NUMBER: US/10/295,723
CURRENT FILLNG DATE: 2000-01-09
FRICK APPLICATION NUMBER: US 60/123,547
FRICK APPLICATION NUMBER: US 60/123,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 YEKKPPKEFLERFKSLLQKMIHQHLS 153
121 YEKRTPKEFLERLKWLLOKMIHOHLS 146
                                                                                                                                         Sequence 47, Application US/09825561A Parent No. US20020137677A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Mus musculus US-09-825-561A-47
```

```
68 ETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 ETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MERTLYCLVVIFLGTVAHKSSPQGPDRLLIRLRHLIDIVEQLKIYENDLDPELLSAPQDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MERTLYCLVVIFLGTVAHKSSPQGPDRLLIRLRHLIDIVEQLKIYENDLDPRLLSAPQDV 60
                                                                                                                                                                                                                                                                                                                                                                                                            8 MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPBFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.2%; Score 486; DB 15; Length 146; Best Local Similarity 63.0%; Pred. No. 6.6e-45; Matches 92; Conservative 23; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                    Query Match

57.2%; Score 486; DB 14; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Nelson, Andrew J.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: USE OF IL-21 IN CANCER AND TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS FILE REFERENCE: 03-08
CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
PRIOR FILING DATE: 2002-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YEKRTPKEFLERLKWLLOKMIHOHLS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YEKRTPKEFLERLKWLLQKMIHQHLS 146
                                                                                                     NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 146
                           CLING DATE: 1999-03-11
PPLICATION NUMBER: US 60/142,013
CLING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Mus musculus
US-10-456-780-4
                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: mus musculus
US-10-295-723-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

Search completed: March 3, 2004, 12:50:52 Job time: 22.1765 secs

	Ltd.
5.1.6	Compugen
ē	- 2004
enCore	1993
Ger	Û
	Copyright

,
1
1
;

Run on:

March 3, 2004, 12:24:04; Search time 38:6471 Seconds (without alignments) 1184.377 Million cell updates/sec

Title: Perfect score:

US-09-825-561A-10 850 1 MRSSPGNMERIVICLMVIFL......LLQKWIHQHLSSRTHGSEDS 162

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 29Jan04:* L: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab18623 A human z	Aae13729 Human sol	Human	Abr61407 Human IL-	Human i		Ade85808 Human int	Aae14934 Human int		Aab18627 Amino aci	Aaul1971 MBP-human	-	Aae13737 Murine so	_		_	Ade85806 Murine in	Ade85807 Murine in		-	972	Aab18625 Antigenin	696	62	Aaul1970 Human zal
ΠD		AAE13729	AAU11965	ABR61407	AAE14932	ABU62893	ADE85808	AAE14934	AAE14933	AAB18627	AAU11971	AAB18624	AAE13737	AAU11968	ADE85809	ADE85818	ADE85806	ADE85807	ADE85820	AAB18628	AAU11972	AAB18625	AAU11969	AAB18626	AAU11970
th DB	62 3		62 5		7		7 2	-	17 7	519 3	5		9			379 7	16 7	16 7		10 3	0	0	0		C)
Length	ן ה	16	7	16	16	16	16	16	14	51	51	14	14	14	14	W	14	Ä	Ę	53	2	•	7		
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	0	97.8	89.2	81.8	81.8	57.2	57.2	57.2	57.2	57.2	56.6	56.0	56.0	46.4	46.4		•		•
Score	850	850	850	850	850	850	850	831	758	σ	695.5	486	486	486	486	486	481	7	476	394	6	Н	212	7	7
Result No.	-	(1)	m	4	Ŋ	9	7	80	đ	10	11	12	13	14		16		18		20				24	

~ 10 # # C 10 C ~ C ~ C ~ C ~ C ~ C ~ C ~ C ~ C ~ C	Aaw37369 Wild-type Aaw39185 Simian ep
7 ADE85813 AAV54825 AAAC66928 2 AAR66928 2 AAR66928 2 AAW070253 AAR831186 AAW37186 2 AAW37186 3 AAX6213 3 AAX6213 2 AAR69213 2 AAR69213 2 AAR69227 2 AAR96227 2 AAR96227 2 AAR96227 2 AAR96227 2 AAR96227 2 AAR96227 2 AAR96227	2 AAW37369 2 AAW39185
25 135 135 135 135 135 144 111 144 162 162 162 162 162	162
	5 11.7
11 10 10 10 10 10 10 10 10 10 10 10 10 1	96
	4 4 4 0

ALIGNMENTS

A human zalphall ligand polypeptide. AAB18623 standard; protein; 162 AA. 22-JAN-2001 (first entry) AAB18623;

ell proliferation; lymphoma; cell tumour zalphall ligand; cytokine; haematopoletic cell tumourigenesis; leukaemia; hematopolesis; B cel

Homo sapiens.

WO200053761-A2.

14-SEP-2000.

09-MAR-2000; 2000WO-US006067.

99US-00264908. 99US-00265992. 99US-0142013P. 09-MAR-1999; 11-MAR-1999; 01-JUL-1999;

(ZYMO) ZYMOGENETICS INC.

Foster DC, Holly RD; 11on SR, Hammond AK; Sprecher CA, Foster DC, Nelson AJ, Dillon SR, Novak JE, Presnell SR, Gross JA, Johnston JV,

WPI; 2000-565600/52. N-PSDB; AAA75552.

New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of hematopoletic cells in vitro and in vivo, and for treating tumorigenesis.

Disclosure; Page 205-206; 256pp; English.

The present sequence represents a human zalphall ligand polypeptide, which is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of hematopoletic cells in vitro and in vivo. Zalphall ligand polynucleotides can be used as primers or probes for cloning the zalphall igene. The zalphall ligand is useful for treating trumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemiss and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion,

Nelson AJ

Holly RD,

```
ö
                                                                                                                                                                                                                                                                LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                   61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic; inflammatory disorder; haemostatic; cell proliferation; immune disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma; ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis; viral infection.
                                                                                                                                                                                                                                  9
proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimmlate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                        1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                    1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                            Gaps
                                                                                                                                                                            .
0
                                                                                                                                              Length 162;
                                                                                                                                                                            IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human soluble Zalphall cytokine receptor ligand protein.
                                                                                                                                                                                                                                                                                                                                             TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                            TCPSCDSYEKKPPKEFLERPKSLLQXMIHQHLSSRTHGSEDS 162
                                                                                                                                               100.0%; Score 850; DB 3;
100.0%; Pred. No. 1.3e-86;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12. 162
|Jabel= Mature_Zalphall_ligand
41. 56
|Jabel= Helix_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Conserved region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .31
label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                AAE13729 standard; protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69. .84
/label= Helix_B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Helix_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135. .148
/label= Helix_D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2000; 2000US-0194731P.
28-JUL-2000; 2000US-0222121P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-2001; 2001WO-US010872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....138
/note= "C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                               Sest Local Similarity 100. Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                     Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200177171-A2
                                                                            prevention, and
genetic defect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001
                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13729;
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                   AAE13729
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             888888888
                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                             ਨੇ
```

```
The invention relates to an isolated soluble zalphall cytokine receptor polypeptide and their cDNA molecules. Zalpha proteins are useful for inhibiting or antagonialing the ligand activity-induced proliferation of haematopoietic cells and haematopoietic cell progenitors preferably completed cells which are natural killer cells or cytocoxic T cells. Zalpha is useful for treating immune and inflammatory disorders, for reading proliferation of neoplastic B or T cells, for suppressing an immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthritis, multiple solerosis, myasthenia gravis, systemic lupus erythematosus (SIE) and diabetes; sething understive collisis, inflammatory bowel disease, Crohn's disease, sepsis, viral infection (dengue virus infection) and cancer. The present sequence is human soluble Zalphail cytokine receptor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKFPSTNAGRROKHKL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                    Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRSSPGNMERIVICIMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRWRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; beall proliferation; anti-tumour response; immune system; immunostimulant; cytostatic; human; hPBCS; activated human peripheral blood cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TCPSCDSYEXXPPKEFLERFXSLLQXMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TCPSCDSYEKKPPKEFLERFKSLLOKMIHOHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 850; DB 5; 100.0%; Pred. No. 1.3e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32. .162
/label= Mature_zalpha11_Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .31
/label= Signal_peptide
32. .162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU11965 standard; protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human zalphall Ligand polypeptide.
                                                                                                                                                              Claim 1; Page 181; 243pp; English.
   West JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100,
Matches 162; Conservative
   Novak JE,
                                    WPI; 2002-025898/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                       N-PSDB; AAD22923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6307024-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-2002
 Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU11965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU11965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ጵ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ठ
```

```
New zalphall ligand polypeptides and polynucleotides, useful for
stimulating proliferation, activation, differentiation and/or indo
of inhibition of specialized cell function, or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Col 125-126; 105pp; English
09-MAR-2000; 2000US-00522217
                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                     WPI; 2002-040208/05
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS20637
                                                 09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                   Novak JE,
Gross JA,
```

The present invention relates to the isolation of a novel cytokine, calphall Ligand and the polynucleotide encoding it. The invention also gives the sequence for the zalphall inceptor and the polynucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation of natural killer (NK) cells or NK cells progenitors, the activation of NK cells, proliferation of Teclls, proliferation of Secolls stimulated with anti-CD40 antibodies, stimulates an antiganic response in a mammal, and reduces proliferation of B-cells stimulated with anti-CD40 antibodies the calphall Ligand polypeptide is also useful in preparing antibodies the bind to zalphall Ligand polypeptide is also useful in preparing antibodies that bind to zalphall Ligand polypeptide is also useful in preparing antibodies that be used as probes or primers to clone regions of a zalphall Ligand gene, and in gene therapy. Zalphall Ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence represents human zalphall Ligand polypeptide. The cDNA encoding this is isolated trom a cDNA library from activated human peripheral blood cells (BPECS) Sequence 162 AA;

LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120 9 9 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPRF LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNER!INVSIKKLKRKPPSTNAGRROKHRL Gaps ö Query Match
100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0 61 61 121 셤 ઠે ઠે 8

ABR61407 standard; protein; 162 AA ABR61407 RESULT

12-AUG-2003 (first entry) ABR61407;

Human IL-21 SEQ ID NO:19.

2×5×5×5×5×5

immune cell activity, cancer; infectious disorder; antirheumatic; antiarthritic; osteopathic; antipsoriatic; cytostatic; antibacterial; virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological; neuroprotective; antiulcer; antiallergic; antianaemic; hepatotropic; arthritic disorder; interleukin-21;

autoimmune disease; human

WO2003028630-A2

04-OCT-2002; 2002WO-US029839

Hammond AK;

Sprecher CA, Foster DC, Nelson AJ, Dillon SR, H

Presnell SR, Johnston JV,

99US-0123547P. 99US-0123904P. 99US-0142013P.

04-OCT-2001; 2001US-00972218. 17-APR-2002; 2002US-0373746P

(AMHP.) WYETH.

Young DA, Larsen Ma M, Witek JS, Colling M, Dunussi K, Carter L, Donaldson I Ungar M;

2003-430146/40. N-PSDB; ACC80873 Treating or preventing arthritic disorder, cancer or infectious disorders in a subject, involves administering a modulator of interleukin-21 or its receptor which modulate immune cell activity.

Disclosure, Page 37, 176pp, English

The invention relates to a novel method for treating or preventing an arthritic disorder in a subject. The method involves administering to the arthritic disorder in a subject. The method involves administering to the subject an interleukin-21 (IL-21)/IL-21 Respect (IL-2R) antagonist context of an infectious disorder, in a subject, by administering IL-21/IL-21R agonist, to increase immune cell activity. The action of the invention has antirheumatic, antiarthritic, osteopathic, method of the invention has antirheumatic, antiplarasitic, immunosuppressive, antidiabetic neuroprotective, dermatological, antidiabetic neuroprotective, dermatological, antidiabetic neuroprotective, dermatological, antituloer, antisathmatic, antidiabetic neuroprotective, dermatological, antidiabetic neuroprotective, dermatological, antidiabetic neuroprotective, dermatological, antidiabetic neuroprotective, dermatological, cartifitis, juvenile rheumatory activity. The method of a useful for arthritis or ankylosing spondylitis, and also cancer such as rheumatoid arthritis, osteoritic arthritis, juvenile rheumatoid arthritis, osteorituin and antigen to preferably human. A method of the invention is also useful for increasing the ability of a vaccine composition containing an antigen to elicit a protective immune response in a subject against the antigen to from cancer or tumour cell antigen or expressed on the marker of gancer coll antigen nor expressed on the marker or prevent a curious of immune or hematogonistic cells and thus to reprevent a context of immune of membrase and a such as arrived or prevent and antigen or immune or hematogonistic cells and thus to reprevent antigen of immune or hematogonistic cells and thus to reprevent antigen or membrase for any antigen and antige diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia, hepatitis, Graves's disease, graft versus host disease, and scleroderma. The present sequence is used in an exemplification of the invention immune disorders, such as autoimmune diseases,

Sequence 162 AA;

0; Gaps Length 162; 0; Indels 100.0%; Score 850; DB 6; 100.0%; Pred: No. 1.3e-86; ive 0; Mismatches 0; Matches 162; Conservative Local Similarity

1 WRSSPCNWERIVICLMVIFLGTLVHKSSSQCQDRHMIRMRQLIDIVDQLKNYVNDLVPRF 60 ** 1 MRSSPGWARTUVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPFF.60

8 8

rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopses, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 (originally designated zalphall ligand)

inflammatory and autoimmune disorders, including

such as

162

₹

```
New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides and polypeptides of interleuki 21 (II-21) antagonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D helix of the IL-21 molecule, and can be used to o inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide,
                                                                                                                                                                autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; diabetes; human; zalphall ligand.
TOPSODSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS
               TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 53-54; 71pp; English
                                                                              AAE14932 standard; protein; 162
                                                                                                                                                   Human interleukin-21 (IL-21)
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-441547/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD47852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003040313-A2
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                           Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                           27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LS-MAY-2003
                                                                                                    AAE14932;
121
                     121
                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                    AAE14932
                                                         RESULT
                                                                                                                g
ò
```

```
note= "Important for IL-21 binding to its receptor"
                                                         note= "Important for IL-21 binding to its receptor"
                                                                                    for IL-21 binding to its receptor"
Location/Qualifiers
                                                                                      note= "Important
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Presnell SR, West JW, Novak JE
                                                                                                                                                                            B/C_100p
                                                                                                                                                                                                                                        C/D_loop
                                                                                                                  .abel= A/B_loop
              41. .56
/label= Helix_A
                                                                                                                                                                                                          Helix_C
                                                                                                                                                                                                                                                     135. .148 __/
/label= Helix_D
                                                                                                                                               Helix_B
                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-2002; 2002WO-US034502.
                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001; 2001US-0337586P.
                                                                                                                                                                                                                       /label= C/i
                                                                                                                                                                                            2. .105
label= H
                                                                                                                                 9. .84
label= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                             5. .91
|abel=
                                                                                                      .68
```

```
ö
                                                                                                                                                                                                                                                                                                   61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                       LPAPEDVETNCEWSAFSCPOKAQLKSANTGNNERLINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator; cytostatic; antibacterial; virucide; antianaemic; gene therapy; haematopoiesis; anaemias; immune response; cancer; infection; transplanted organ; cytokinis; receptor; incerleukin. 21; IL21;
                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                          MRSSPGNMERIVICLMVIFLGTLVHKSSSQGDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                               MRSSPGNMERIVICLMVIPLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                             Gaps
                                                                                                                                                                                             .
                                                                                                                                                          Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nlating hematopolesis and in polypeptide and a non-MU-1
                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                            TCPSCDSYEKKPPKEFLERPKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                        Query Match
100.0%; Score 850; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.36-86;
Matches 162; Conservative 67; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 10, 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L, Whitters MJ, Collins
J, Unger M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment of a MU-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human interleukin 21 (IL-21):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2000; 2000US-00560766
11-MAY-2000; 2000US-00569384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2001; 2001US-00972218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00040005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion polypeptide for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003049798-A1 : 00 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YOUNG D.A.
DONALDSON D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-512354/48.
N-PSDB; ACD26729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLINS M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOWE L D.
UNGER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARTER L. WHITTERS N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                       Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU62893;
                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter L. Lowe LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU62893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DONA/)
(LOWE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU6289
8888888
                                                                                                                                                                                                                                                                                                     ठ
```

interleukin-

```
The invention describes a fusion polypeptide comprising at least a fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The polypeptide is useful in regulating haematopoises (e.g. in cases of anaemias) and/or immune responses (e.g. immune response to cancer, infections or to a transplanted organ) and in identifying other members of the haematopoistin superfamily, including otherines and receptors. The polymucleotide may be used to express recombinant protein for analysis, characterisation or therapeutic use; and as markers for tissues or chromosomes. The polypeptide and polymucleotide may also be used as nutritional sources or supplements. This is the amino acid sequence of human interleukin 21 (IL21), a cytokine receptor that can be used to characterise the novel haematopoietin receptor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the protein sequence of human interleukin-21 (IL-21). The invention provides antagonists of the IL-21 receptor. These include mutants of murine IL-21 in which the Gln residue at position 119
                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New substantially pure interleukin-21 polypeptide, useful for diagnosing, treating and prognosticating autoimmune disorders, e.g. rheumatic disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis and myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-21; immunosuppressive; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                            1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGDDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                               1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGODRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; dermatological; ophthalmological; uropathic; muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic; neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy
                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                100.0%; Score 850; DB 7; Length 162; 100.0%; Pred. No. 1.3e-86; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 1; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE85808 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEACONESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng XX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-2003; 2003WO-US010736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-2002; 2002US-0371038P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interleukin-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BETH-) BETH ISRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-845317/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strom TB,
                                                                                                                                                                                                                                                          Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003087320-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE85808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moll T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE85808
      8866666666666888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
residues at positions 114 and 119 of the mature polypeptide are both replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell activation. They preferably comprise a sequence that increases circulating half-life, such as the Fc region of an IgG molecule and may proliferation in response to either anti-CD3 monoclonal antibodies or proliferation in response to either anti-CD3 monoclonal antibodies or IL-21. A claimed method of suppressing the immune response in a patient comprises administering the IL-21 antegonist or ancieto acid encoding it. The method is used to treat an autoimmune disease such as rheumatic cliease, including systemic lupus erythematosus, Sjogran's syndrome, selectoderma, mixed connective tissue disease, dermatomyositis, polymyositis, Reiter's syndrome, or Behcet's disease, or rheumatoid surhritis, type I diabetes, autoimmune disease, or rheumatoid surhritis, type I diabetes, autoimmune disease of the central nervous system such as multiple sclerosis, myasthenia gravis, or encephalomyelitis, or an autoimmune disease elected from pemphigus vegetans, pemphigus foliaceus, Senear-Usher syndrome, selectal in pemphigus vegetans, pemphigus for inflammatory bowel disease (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERI INVSIKKLKRFPSTNAGRRQKHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-21; IL-21; antagonist; cancer; inflammatory; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; diabetes; human; zalphall ligand; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 850; DB 7; Length 162; 100.0%; Pred. No. 1.3e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Wild-type Gln substituted with Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Ile substituted with Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interleukin-21 (IL-21) antagonist #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE14934 standard; protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001; 2001US-0337586P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-2002; 2002WO-US034502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003040313-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE14934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

```
The invention relates to polynucleotides and polypeptides of interleukin-
[11-21] antagonists, that bind with specificity and exhibit an BC50
[11-21] antagonists, that bind with specificity and exhibit an BC50
[11-21] antagonists in receptor binding studies. The antagonists of
[11-21] antagonists are useful for diagnoshing and treating disorders
[11-21] antagonists are useful for diagnoshing and treating disorders
[11-21] antagonists are useful for diagnoshing and treating disorders
[11-21] antagonists are useful for adagnoshing and treating disorders
[11-21] antagonists are useful for adagnoshing and treating disorders
[11-21] polypeptides
[11-21] polypeptides
[11-21] antagonist and diabetes. The polypeptides or polypeptides
[11-21] antagonist and diabetes. The polypeptides or polypeptides
[11-21] antagonist and diabetes are tracet tissues. The present sequence
[11-21] antagonist. The antagonist molecule is a mutant of IL-21
[11-21] polypeptide, with Gln145Asp and Ile148Asp substitutions. The resulting
[11-21] mutant was designated zalphall ligand Q153D/II56D
                                                                                                                                              New IL-21 polypeptide and encoding polynuclectide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPAPEDVETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRPPSTNAGRROKHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-21; IL-21; antagonist; cancer; inflammatory; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; diabetes; human; zalpha11 ligand; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TCPSCDSYEKKPPKEFLERFKSLLDKMDHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-21 (IL-21) antagonist #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE14933 standard; protein; 147 AA
                                          Novak JE;
                                                                                                                                                                                                                                                     Claim 3; Page 58; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.1%;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
(ZYMO ) ZYMOGENETICS INC
                                        Presnell SR, West JW,
                                                                                  WPI; 2003-441547/41
                                                                                                      N-PSDB; AAD47854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE14933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE14933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
The invention relates to polynucleotides and polypeptides of interleuking that integonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D halix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The invention have mutations in the D halix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide, such as cancer, inflammatory and autoimmume disorders, including the under the pression of a systemic lugus erythematosus, mysthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 antagonist. The antagonist molecule is a mutant of IL-21 polypeptide, with truncation after residue 147 (Met) and GIL-21 polypeptide, with truncation after residue 147 (Met) and GIL-21 polypeptide.
                                                                                                                                                                                                                                                                      New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis; multiple sclerosis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAPEDVETNCEWSARSCFOKAOLKSANTGNNERIINVSIKKIKRKPPSTNAGRROKHRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zalphall ligand, cytokine, haematopoietic cell proliferation, lymphoma;
tumourigenesis, leukaemia; hematopoiesis; B cell tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDSSPGNMERIVICIMVIFIGTLYHKSSSQGDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of MBP-human zalphali ligand fusion in pTAP126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.2%; Score 758; DB 7; Length 147; 98.6%; Pred. No. 2.2e-76; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCPSCDSYEKKPPKEFLERFKSLLDKM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCPSCDSYEKKPPKEFLERFKSLLQKM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18627 standard; protein; 519 AA.
                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 55-56; 71pp; English.
                                                                                                                                                                   Novak JE;
                                        28-OCT-2002; 2002WO-US034502
                                                                                  05-NOV-2001; 2001US-0337586P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 145; Conservative
                                                                                                                                                                   Presnell SR, West JW,
                                                                                                                         (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                           WPI'; 2003-441547/41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                             N-PSDB; AAD47853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200053761-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1156ST/Q153D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JAN-2001
15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB18627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18627
쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

120 120

/note= "Wild-type Gln substituted with Asp"

Location/Qualifiers

Misc-difference 145

WO2003040313-A2

9 60

Gaps

ó

3; Indels

Score 831; DB 7; Length 162; Pred. No. 1.7e-84;

ô

9 9

09-MAR-2000; 2000WO-US006067,

14-SEP-2000

```
The present sequence represents a MBP-human zalphall ligand fusion in the plasmid pTAP126. Zalphall ligand is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of haseful for stimulating the proliferation and development of hasematopoietic cells in vitro and in vivo. Zalphall ligand polymucleotides can be used as primers or probes for cloning the zalphall appears in the zalphall ligand is useful for treating tumourispensis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoissis. The zalphall ligand may also be used to stimulate an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 LVPRGS---QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA 439
                                                                                                                                                                                                                                                                                                                                                                     New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of hematopoietic cells in vitro and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand genetic defect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 LVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCPQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 QLKSANTGNNERLINVSIKKLKRPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; mutant; B-cell proliferation; anti-tumour response; immune system; MBP; immunostimulant; cytostatic; human; maltose binding protein; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 695.5; DB 3; Length 519;
Pred. No. 1.1e-68;
1; Mismatches 2; Indels 3
                                                                                                                                                                                                                                        , Foster DC, Holly RD;
Dillon SR, Hammond AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBP-human zalphall Ligand fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 31; Page 233-235; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   in vivo, and for treating tumorigenesis.
                                                                                                                                                                                                                                        Sprecher CA,
Nelson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU11971 standard, protein, 519 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLOKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 LLOKMIHOHLSSRIHGSEDS 519
                                                                                                      99US-00264908.
99US-00265992.
99US-0142013P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.7%;
Matches 134; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2002 (first entry)
                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                     Novak JE, Presnell SR, Gross JA, Johnston JV,
                                                                                                                                                                                                                                                                                                        WPI; 2000-565600/52
                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA75599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 519 AA;
                                                                                                      09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU11971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU11971
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
The present invention relates to the isolation of a novel cytokine, albhali Ligand and the polymucleotide encoding it. The invention also gives the sequence for the zalphali receptor and the polymucleotide encoding it. The zalphali receptor and the polymucleotide encoding it. The zalphali Ligand polypeptide stimulates proliferation of natural killer (WK) cells or NK cell progenitors, the activation of NK cells, proliferation of B-cells or NK cells proliferation of B-cells simulated with anti-Co40 antibodies, stimulates an antigenic response in a mammal, and reduces proliferation of B-cells stimulated with anti-fod antibodies. The bind to zalphali Ligand epitopes. The zalphali Ligand polypucleotides can be used as probes or primers to clone regions of a zalphali Ligand gene, and in gene therapy. Zalphali Ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 OLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDSYEKKPPKEFLERFKS 499
                                                                                                                                                                                                                                                                                                                                                                                                                                       New zalphall ligand polypeptides and polymucleotides, useful for
stimulating proliferation, activation, differentiation and/or induction
of inhibition of specialized cell function, or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 LVPRGS----QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 QLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDSYEKKPPKEFLERFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 LVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activate or stimulate the immune system. The present sequence representing MBP-human zalphall Ligand fusion protein is used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%; Score 695.5; DB 5; Length 519; 95.7%; Pred. No. 1.1e-68; 1.4ve 1; Mismatches 2; Indels 3.
                                                                                                                                                                                                                                                                                                                    Sprecher CA, Foster DC, Holly RD;
Nelson AJ, Dillon SR, Hammond AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 31; Col 161-166; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB18624 standard; protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 LLOKMIHOHLSSRIHGSEDS 519
                                                                                                                                                                                             99US-0123547P.
99US-0123904P.
99US-0142013P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLOKMIHOHLSSRTHGSEDS
                                                                                                                                                         09-MAR-2000; 2000US-00522217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 95.7
Matches 134; Conservative
                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                    Presnell SR,
Johnston JV,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-040208/05.
N-PSDB; AAS20714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 519 AA;
                                                                                                                                                                                             09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2001
                                                                            US6307024-B1
                                                                                                                  23-OCT-2001
                                                                                                                                                                                                                                                                                                                  Novak JE,
Gross JA,
                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
AAB18624
ID AAB18
XX
AC AAB18
XX
DT 22-JA
ò
```

142 439

82

499

82

3,

us-09-825-561a-10.rag

```
Murine, Zalphall; cytokine receptor; immunosuppressive; cytostatic; inflammatory disorder; haemostatic; cell proliferation; immune disorder; autoimmune disease; rehumatoid arthritis; multiple sclerosis; cancer; myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma; ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel soluble receptor polypeptides and polynucleotides used as cytol antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 West JW, Presnell SR; Holly RD,
                                                            Murine soluble Zalphall cytokine receptor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 212; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2000; 2000US-0194731P.
28-JUL-2000; 2000US-0222121P.
                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2001; 2001WO-US010872
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sprecher CA, Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-025898/03.
N-PSDB; AAD22952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 146 AA;
                                                                                                                                                                                                          viral infection
                                                                                                                                                                                                                                                                                           WO200177171-A2.
                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                      18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a mouse zalphall ligand polypeptide, which is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of haematopoletic cells in vitro and in vivo. Zalphall ligand polymucleotides can be used as primers or probes for cloning the zalphall ligand saporin fuach croxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand to reacting leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite con a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, contention, and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of hematopoietic cells in vitro and in vivo, and for treating tumorigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MERTLVCLVVIFLGTVAHKSSPQGPDRLLIRLRHLIDIVEQLKIYENDLDPELLSAPQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRRPPSTNAGRRQKHRLTCPSCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                         , Foster DC, Holly RD;
Dillon SR, Hammond AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 57.2%; Score 486; DB 3; Length 146; Similarity 63.0%; Pred. No. 5.6e-46; 92; Conservative 23; Mismatches 31; Indels
                                                          zalphall ligand; cytokine; haematopoietic cell prolifer
tumourigenesis; leukaemia; hematopoiesis; B cell tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 222-223; 256pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEKKPPKEFLERFKSLLQKMIHQHLS 153
                                                                                                                                                                                                                                                                                                                                                                                                                         Sprecher CA,
Nelson AJ, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEKRIPKEFLERLKWILQKMIHQHLS
               A mouse zalphall ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13737 standard; protein; 146 AA
                                                                                                                                                                                                                                                                                         99US-00264908.
99US-00265992.
99US-0142013P.
                                                                                                                                                                                                                                                09-MAR-2000; 2000WO-US006067
                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                     Presnell SR,
Johnston JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-565600/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA75580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 146 AA;
                                                                                                                                                           WO200053761-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic defect
                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                         09-MAR-1999;
11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                    01-JUL-1999;
                                                                                                                                                                                                      14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                     Novak JE,
Gross JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
```

cytokine n of

```
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KGHCEHAAFACFQKAKLKPSNPGNNKTFIIDLVAQLRRRLPARRGGKKQKHIAKCPSCDS 120
The invention relates to an isolated soluble zalphall cytokine receptor polypeptide and their CDNA molecules. Zalpha proteins are useful for inhibiting or antagonising the ligand activity-induced proliferation of haematopoietic cells and haematopoietic cell progenitors preferably impublic cells which are natural killer cells or cytotoxic T cells. Zalpha is useful for treating immune and inflammatory disorders, for reducing proliferation of neoplastic Borr cells, for suppressing an immune response in a mammal exposed to an antigen or pathogen. Zalpha is useful for treating diseases that require immune regulation including autoimmune diseases such as rheumatoid arthritis multiple sclerosis; mysthenia gravis, systemic lupus expthematosis (GLB) and diabetes, asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, sepsis, viral infection (dengue virus infection) and cancer The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sepsis, viral infection (dengue virus infection) and cancer. The present sequence is murine soluble Zalphall cytokine receptor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MERTLYCLYVIFLGTYAHKSSPQGPDRLLIRLRHLIDIYBQLKIYENDLDPELLSAPQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 MERIVICLMVIPLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPBFLPAPEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.2%; Score 486; DB 5; Length 146; 63.0%; Pred. No. 5.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEKKPPKEFLERFKSLLOKMIHOHLS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEKRTPKEFLERLKWLLOKMIHOHLS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU11968 standard; protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
AAU11968
ID AAU11
```

Best Loca Matches

ठे 음 셤

AAE13737

RESULT 13 AAE13737

```
Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; B-cell proliferation; anti-tumour response; immune system; immunostimulant; cytostatic; mouse.
                                                                                                Mouse zalphall Ligand polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-2000; 2000US-00522217,
                                              09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novak JE, Presnell SR,
Gross JA, Johnston JV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-040208/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                  US6307024-B1
                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2001
AAU11968;
```

Sprecher CA, Foster DC, Holly RD; Nelson AJ, Dillon SR, Hammond AK;

99US-0123547P. 99US-0123904P.

The present invention relates to the isolation of a novel cytokine, calphall Ligand and the polymucleotide encoding it. The invention also gives the sequence for the Zalphall Enceptor and the polymucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation of matural killer (NK) cells or NK cell progenitors, the activation of NK cells, proliferation of T-cells, proliferation of T-cells, proliferation of T-cells stimulated with anti-CD40 antibodies, stimulates an antigenic response in a mammal, and reduces proliferation of B-cells stimulated with anti-IgM antibodies. The zalphall Ligand polymorphale is also useful in preparing antibodies that bind to zalphall Ligand epitopes. The zalphall Ligand polymucleotides can be used as probes or primers to clone regions of a zalphall Ligand gene, and in gene therapy. Zalphall Ligand may also be used to identify antibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence represents New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an antigenic response. 0; Gaps 57.2%; Score 486; DB 5; Length 146; 63.0%; Pred. No. 5.6e-46; ive 23; Mismatches 31; Indels Example 16; Col 147-150; 105pp; English. mouse zalphall Ligand polypeptide Best Local Similarity 63.03 Matches 92; Conservative N-PSDB; AAS20688. Sequence 146 AA; Query Match

```
61 KGHCEHAAPACFQKAKLKPSNPGNNKTFIIDLVAQLRRRLPARRGGKKQKHIAKCPSCDS 120
                                       68 ETNCEWSAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRROKHRLTCPSCDS 127
8 MERIVICLAMVIFLGTLVHKSSSQGODRHMIRARQLIDIVDQLKNYVNDLVPEFLPAPEDV 67
                                                                                                                                                                                                                                                                   128 YEKKPPKEFLERFKSLLOKMIHQHLS 153
```

121 YEKRTPKEPLERLKWLLOKMIHOHLS 146

```
The present sequence is the protein sequence of murine interleukin-21 (IL 21). The invention provides antagonists of the IL-21 receptor. These include mutants of murine IL-21 in which the GIL residues at position 119 of the mature polypeptide is substituted by Asp ADS8500 or in which the GIL residues at position 114 and 119 of the mature polypeptide are both compared by Asp ADS8507. The mutant IL-21 polypeptides inhibit or suppress T-cell activation. They preferably comprise a sequence that increases circulating half-life, such as the Fc region of an IgG molecule increases circulating half-life, such as the Fc region of an IgG molecule call ary proliferation in response to either anti-CD3 monoclonal call and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full and full 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New substantially pure interleukin-21 polypeptide, useful for diagnosing, treating and prognosticating autoimmune disorders, e.g. rheumatic disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis and myasthenia gravis.
                                                                                                                                                                                                                                                                      antiarthritic
                                                                                                                                                                                                                                                                Mouse, interleukin-21, immunosuppressive, antirheumatic, antiarthrit artiinflammetory, dermatological, ophthalmological, uropathic, muscular-gen,; vasotropic, antidiabetic, antithyroid, thyromimetic, newroprotective, gastrointestinal-gen, antipsoriatic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2; 65pp; English:
                                                      ADE85809 standard, protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-APR-2003; 2003WO-US010736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-2002; 2002US-0371038P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zheng XX;
                                                                                                                                                                                                               Murine interleukin-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-845317/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moll T, Strom TB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003087320-A2.
                                                                                                                                                              29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2003.
                                                                                                       ADE85809;
                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
RESULT 15
ADE85809
```

Query Match
57.2%; Score 486; DB 7; Length 146;
Best Local Similarity 63.0%; Pred. No. 5.6e-46;
Matches 92; Conservative 23; Mismatches 31; Indels Sequence 146 AA; claimed). Query Match

8 MERIVICLANIFICTLYHKESSQQQDRHMIRARQLIDIVDQLKNYVNDLVPEFLPAPEDV 67

```
1 MERTLYCLYVIFLGTVAHKSSPQGPDRLLIRLRHLIDIVEQLKIYENDLDPELLSAPQDV 60
```

g

ò

S 127		S 120
CPSCDS	=	PSCD
NAGRROKHRLTCPSCD	=	KOKHIAK
STNAGRI	··	PARRGGK
KLKRKPF	-:-	7AQLRRLPARRGGKKQKHIAK C
SAFSCFOKAQLKSANTGNNERIINVSIKKLKRKPPSTN		NPGNNKTFI IDLVA(
NTGNNER	=	NPGNNKT
CAQLKSA	 	SHCEHAAFACFOKAKLKPSNI
AFSCFOF	= = =	AFACFOR
68 ETNCEWS	 	KGHCEHA
89		61

ò

q

Search completed: March 3, 2004, 12:35:39 Job time : 39.6471 secs